

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 10:57:38 ; Search time 225 Seconds
(without alignments)
7916.075 Million cell updates/sec

Title: US-10-088-726-25
Perfect score: 1002
Sequence: 1 atggagaggtggacatgaa.....ggttgaacagatctgggtaa 1002

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/pp COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	229.4	22.9	2025	US-09-016-434-1482	Sequence 1482, Ap
2	229.4	22.9	2025	US-09-814-915A-74	Sequence 74, Appl
3	205.4	20.5	1842	US-08-442-134A-1	Sequence 1, Appli
4	205.4	20.5	1842	US-08-444-581B-1	Sequence 1, Appli
5	205.4	20.5	1842	US-08-446-088A-1	Sequence 1, Appli
6	180.2	18.0	1429	US-09-016-434-1068	Sequence 1068, Ap
7	180.2	18.0	1429	US-09-077-173D-1	Sequence 1, Appli
8	166.4	16.6	984	US-08-513-974B-57	Sequence 57, Appl
9	166.4	16.6	984	US-09-461-436B-57	Sequence 57, Appl
10	166.4	16.6	1023	US-08-513-974B-379	Sequence 379, App
11	164.8	16.4	1571	US-09-016-434-1108	Sequence 1108, Ap
12	158.4	15.8	984	US-08-459-046-1	Sequence 1, Appli
13	158.4	15.8	984	US-09-102-710B-1	Sequence 1, Appli
14	150.4	15.0	984	US-08-513-974B-41	Sequence 41, Appl
15	150.4	15.0	984	US-09-461-436B-41	Sequence 41, Appl
16	150.4	15.0	1020	US-08-513-974B-370	Sequence 370, App
17	99	9.9	1119	US-09-826-509-538	Sequence 538, App
18	99	9.9	1773	US-09-016-434-1405	Sequence 1405, Ap
19	97.4	9.7	998	US-08-432-174A-3	Sequence 3, Appli
20	94	9.4	1892	US-09-900-699A-1	Sequence 1, Appli
21	93.6	9.3	1475	US-08-097-938-1	Sequence 1, Appli
22	93.6	9.3	1475	US-08-476-000-1	Sequence 1, Appli
23	93.6	9.3	1475	US-08-472-840-1	Sequence 1, Appli
24	93.6	9.3	1475	US-08-476-976-1	Sequence 1, Appli

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Sequence 60, Appl
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Sequence 60, Appl
Sequence 568, App
Sequence 60, Appl
Sequence 13, Appl
Sequence 1, Appli
Sequence 1302, Ap
Sequence 1456, Ap
Sequence 31, Appl
Sequence 181, App
Sequence 1484, Ap
Sequence 43, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-016-434-1482
; Sequence 1482, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1482:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2025 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g984506
US-09-016-434-1482

1/30/98 Jurd.
1/27/02 JS.

Db 1095 ATCAACATGGCGCTACAGGTTACCGCGCGCTGGCCAGTGTCTAACAGTTGCTTGAACCCC 1154
Qy 878 GTCTGTACTTCTTTCAAGG 898
Db 1155 GTGCTCTACTTCTCGGTGGG 1175

RESULT 3

US-08-442-134A-1
; Sequence 1, Application US/08442134A
; Patent No. 5596088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
US-08-442-134A-1

Query Match 20.5%; Score 205.4; DB 2; Length 1842;
Best Local Similarity 56.4%; Pred. No. 5e-45;
Matches 486; Conservative 0; Mismatches 361; Indels 14; Gaps 5;
Qy 43 TCCAGTCTCTAGAGATGACAGGTTACCTCTCGCTGGCCCTACAGTATCATCTTT 102
Db 129 TGCCGCTTCAAGAGGACTTCAAGTACGCTGTCTGCTGCTGTCTACGCGGTGGTGTGC 188
Qy 103 ATCTTAGGGCTCCCACTAAATGGCACTGTCTTGTGGCACTCTCGGGGCAAAACCAAGCGC 162
Db 189 GTGCTTGGGCTGTGTCTGAACCCCGCTGTACATCTTCTTGTGGCGCTCAAGACC 248
Qy 163 TGGAGCTGTGCCACCACTATCTGGTGAACCTGTAGTGTGGCGGACCTGCTTTATGTGCTA 222
Db 249 TGGAAATGCGTCCACCAATATATGTTCCACCTGGCTGTCTGTGATGCACTGTATGGCGCC 308

Qy 223 T---TGCCCTTCTCATCATCACTACTACTAGTAGACAGGTGGCCCTTCGGGGAGCTG 279
Db 309 TCCTTGGCGCTGTGTGCTATTACTAGCCCGCGCGACCACTTGCCCTTCAGCACGGTG 368
Qy 280 CTCTGCAAGCTGTGTGCTATCTATATCAACCTTTATACGGCAGCATCTCTGCTGTG 339
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Db 489 GGGCGGGCCGCTACGCTCGCGGGTGGCGGGCGGTGTGGG---TGTGGTGTGGCC 545
Qy 460 CTGTGCGCCACATGTGGCTTCTCCCAACGAGCATCATCAATATGCGCAGATCTGTAT 519
Db 546 TGCAGGCGCCGCTGTCTACTTTGTCAACCAACGCGCGGGCGGCTAACCTGCCAC 605
Qy 520 GACATGACCAAGCAAGAGATTTGATCGGCTTTTTCGCTACGGCATAGTTCTGACATTG 579
Db 606 GACACCTCGGACCCGAGCTCTTACGCGCTTCTGCGCTTACAGCTCATGCTGCGGC 665
Qy 580 TCTGGCTT---TCTTTCCTCTCTGCTGCTATTTGGTGTGCTATTCACTGATGGTCAGGAGC 637
Db 666 CTGCTCTTGGGGTGGCTTTCGCGTCTCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 725
Qy 638 CTGATCAAGCCAGAGAGAACCTCATGAGCAGGCAACAGCCCGAGCCAGGTCCATC 697
Db 726 CTGCTAAAGCCAGCTACGGGACCTCGGGGGCGCTGCTAGGGCAAGCGCAAGTCCGCTG 785
Qy 698 CGGACCATCTACTGTGTGTGGCTCTTCACTCTGTTTGTGGCTTCCATATCACT 757
Db 786 CGCACCATCGCGGTGTGTGGCTCTTTCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
Qy 758 CGCTCTTCTACCTCACCATCTGCTTCTGCTGCTTCTCAGGACTGCCAGCTCTTGTATGCA 817
Db 846 CGACCTCTACTACTCTTCTCGCT---CGCTGACCTCAGCTGCCACACCTCAACGCC 902
Qy 818 GCCAGTGTGGCTCAAGATATGAGGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 877
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Qy 878 GTCTGTACTTCTTTCAAGG 898
Db 960 GTGCTCTACTTCTGGCTGGG 980

RESULT 4

US-08-444-581B-1
; Sequence 1, Application US/08444581B
; Patent No. 5607836
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5607836th Carolina
; COUNTRY: USA
; ZIP: 28234

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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,581B
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/442,134
; FILING DATE: 16-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-444-581B-1

Query Match 20.5%; Score 205.4; DB 2; Length 1842;
Best Local Similarity 56.4%; Pred. No. 5e-45;
Matches 486; Conservative 0; Mismatches 361; Indels 14; Gaps 5;

QY 43 TGCCAGTCTTCAGAGAAGTACAAAGTCTACCTCTCCCTGGCTACAGTATCATCTTT 102
DB 129 TGCCGCTTCAAGAGGACTCAAGTACGTGCTGCTGTCTGTCTTCTAGGGGTGGTGC 188
QY 103 ATCTAGGGCTGCCACTTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGC 162
DB 189 GTGCTTGGGCTGTCTGTAAGCGGCTGCGGCTCTACATCTTCTTGTGCGGCTCAAGACC 248
QY 163 TGGAGCTGTGCCACCACCTATCTGGTGAACCTGATGTGGCGGACCTGCTTATGTGCTA 222
DB 249 TGGAAATCGTCCACCACATATATGTTCCACCTGGCTGTCTGTATGACACTGTATGCGGCC 308
QY 223 T---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTTCGGGGAGCTG 279
DB 309 TCCCTGCGGCTGTGGTCTATTACTAGCGCGGGGACCACTGGCCCTTTCAGCAGGCTG 368
QY 280 CTCTGCAAGCTGTGTGCACTTCTCTGTCTATATCAACCTTTACGGCAGCATCCTGCTGCTG 339
DB 369 CTCTGCAAGCTGTGTGCGCTTCTCTCTCTACACCAACCTTTACTGACGATCCTCTTCTC 428
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QY 400 CGGACCCGCGGAGTCTGCTGGGACCAAGCAACCACTGGGCGCTGTGCTCTCCAG 459
DB 489 GGCGGGCGCGCTACGCTGCGGGGTGGCGGGGCGGTGTGGG---TGTGGTGTGGCC 545
QY 460 CTGCTGCCACACATGGGCTTCTCCACACGAGCTATACATCAATGGCCAGATGATCTGGTAT 519
DB 546 TGCCAGGCGCGGTGCTCTACTTTGTCAACCAAGCGCGCGGCGCTAACCTGCCAC 605
QY 520 GACATGTCAGGCAAGAGATTTTGTATCGGCTTTTGGCTACGGCATAGTCTGACATTTG 579
DB 606 GACACCTCGGACCCGAGCTCTTTCAGCGGCTTGTGGGCTTACAGCTCAGTCTGCTGGGC 665
QY 580 TCTGGCTT---TCTTTCCTCTCTTGGTATTTGGTGTGCTATTCACTGATGGTTCAGGAGC 637
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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,088A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-446-088A-1

US-08-446-088A-1
; Sequence 1, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691156th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,088A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-446-088A-1

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726 CTGCTAAAGCCAGGCTACGGGACCTCGGGGGGCTGCTAGGGCCAAAGCGAAGTCCGTG 785
698 CGGACCATCTACTGTTGTGTCCTTTCACGCTCTGTTTGTGCTTGTGCTTGCATATCACT 757
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758 CGTCTCTTCTACCTCAACATCTGCTTCTTCTCAGGACTGCCAGCTCTTGTATGGCA 817
846 CGACCTCTTCTACTCTCTTCCGCT---CGTGGACCTGAGCTGCCACACCTCAAGCC 902
818 GCCAGTGTGGCTTACAGATATGAGGCTCTTGGTGTGAGTGTGAGAGCTGCCCAACCCA 877
903 ATCAACATGGCTTACAGGT---TACCGGCTGGCCAGTCTAACAGTTGCCTTGACCCC 959
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960 GTGCTCTACTTCTGCTGG 980

RESULT 5
US-08-446-088A-1
; Sequence 1, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691156th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,088A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-446-088A-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753

TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:

LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA
US-08-513-974B-57

Query Match 16.6%; Score 166.4; DB 3; Length 984;
Best Local Similarity 52.1%; Pred. No. 1.1e-34;
Matches 445; Conservative 0; Mismatches 401; Indels 8; Gaps 3;

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Qy	102	TATCTAGGGTCCCAATAGGCACTGTCTTGTGGCACTTCTGGGCGCAAAACCAAGCG	161
Db	111	GGCGCTGGCTGGCTGGCTGACATCTGTGTCTATTACCGAGATCTGCAGTCCCGCGGCG	170
Qy	162	CTGGAGCTGTGCCACCACTATCTGGTGAACTGTAGTGTGGCGCACTGCTTTATGTCT	221
Db	171	CCTGACCGCGCGCGGTGTACACCTAAACCTTCTCTGGCTGACCTGTATATATGCTG	230

Qy	222	AT---TGCCCTTCTCATCATCACTACTACATAGATGACAGGTGGCCCTTCGGGAGCT	278
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Qy	279	GCTCTGCAAGCTGTGCATCTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCT	338
Db	291	CGCTGCGGCTGGTGGCTTCTCTTCTATGCAACCTTGACGGCAGCATCTCTTCTCT	350
Qy	339	GACCTGCATCTCTGTGCACCAAGTTCTAGGTGTGTGGCCACCACTGTGTCTGCTGCCCTA	398
Db	351	CACCTGCATCAGCTTCACGGCTACCTGGGCATCTGCCACCGCTGGCCCTCGGCACAA	410
Qy	399	CC---GGACCCGCGAGGATGCTGGCTGGGCACCAAGCACTGGGCTTGGTGTCT	455
Db	411	ACGTGGGCGCGCGGCTGCTGGCTAGTGTGTAAACCGTGTGGCTGGCGGTGACAA	470
Qy	456	CCAGCTGCTGCCACACTGGCTTCTCCACAGGCACTACATCAATGGCCAGATGATCTG	515
Db	471	CCAGTGGCTGCCACAGCCATCTTGGCTGGCCACAGGCACTCCAGCGTAAACCGCACTG	530
Qy	516	GTATGACATGACAGCAAGAGAAATTTTGATCGGCTTTTGGCTACGCACTAGTCTTGAC	575
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Qy	576	ATTGTCTGGCTTCT--TTCCCTCTTGGTCAATTTTGGTGTGTCTTATTCATGATGGTCAG	633
Db	591	TGTATCGGCTTCTGCTGGCTTGTGCTGGCTTGTGCTGGCTTGTCTCTCTGGCTG	650
Qy	634	GAGCTGATCAAGCCAGAGGAAACCTTCATGAGGACAGGCAACACAGCCCGAGCGAGT	693
Db	651	CCGCTGTGCGCGCAGGATGGCCCGCAGAGCCCTGTGGCCAGGAGCGGCGTGGCAAGGC	710
Qy	694	CATCCGACCATCTACTGTGTGGCTTTCACCTCTTTCACCTCTGTTTGTGCCCTTCCATAT	753
Db	711	GGCCCGCATGGCGGTGTGGCTGTGCTTGGCCATGAGCTTCTGCTCTTTTTCAT	770
Qy	754	CACCTCGCTCTTCTACCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT	813
Db	771	CACCAAGACAGCTTACCTGGCAGTGGCTGGACCGCGGCTGCCCTGCACTGATTGGA	830
Qy	814	GGCAGCAGTGTGGCTTACAGATATGGAGCCCTCTGTGTAGTGTGAGCAGCTGCTCAA	873
Db	831	GGCCTTTGCAAGCGCTTACAAAGGACGCGGCGCTTTGGCAGTGCCACAGCGTCTGGA	890
Qy	874	CCAGTCTCTGACT 887	
Db	891	CCCATCTCTTCT 904	

RESULT 9

US-09-461-436B-57
Sequence 57, Application US/09461436B
Patent No. 6538107

GENERAL INFORMATION:

APPLICANT: Shuji Hinuma

Yasuaki Ito

Ryo Fujii

TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edwards & Angell, LLP

STREET: 101 Federal Street

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-461-436B-57

Query Match      16.6%; Score 166.4; DB 3; Length 984;
Best Local Similarity 52.1%; Pred. No. 1.1e-34;
Matches 445; Conservative 0; Mismatches 401; Indels 8; Gaps 3;

Qy 42 CTGCCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 102 TATCTAGGCTGCCATTAATGCGACTGTCTTGGCACTTCTGGGCGCAACCAACGCG 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 162 CTGGAGCTGTGCCACCACTATCTGTGGAACCTGATGGTGGCCGACCTGCTTTATGTGCT 221
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 171 CTTGACCGGACGCGCGGTACACCCCTAAACCTTGTCTGTGGTACCTGTCTATATGCTG 230
Qy 222 AT---TGCCCTTCTCATCATCATCTACTACTACATAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 231 CTCCTGCCCTGCTCATCTACAACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 290
Qy 279 GCTCTGCAAGCTGGTGCACTTCTGTTCTATATCAACCTTTACGGGAGCATCTCTGCTGCT 338
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 291 CGCTTGGCGCTGGTTCGCTTCTTCTATATGCAACCTGACGCGGAGCATCTCTTCTCCT 350
Qy 339 GACCTGCATCTCTGTGCACCAAGTTCTCTAGGTGTGTGCCACCACTGTGTTCTGCTGCCCTA 398
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 351 CACCTGCATCAGCTTCACGCGTACCTCTGGGCACTCTGCCACCCGCTGGCCCCCTGGCAAA 410
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

399 CC---GGACCCGCGAGGATGCTGCTGGCTGGGCACAGACACCACTGGCCCTGTGTGTCCT 455
411 ACCTGGGGGCGCGCGGCTGCTGGCTAGTGTGTAAACCGTGGCTGGCCGCTGCAAC 470
456 CCAGCTGCTGCCACACACTGCGCTTCTCCCAACAGGACTACATCAATGGCCAGATGATCTG 515
471 CCAGTGGCTGCCACAGCCATCTTCGTGCGCAGGATCCAGGTAACCGCACTGTCTG 530
516 GTATGACATGACGACCAAGAGAAATTTTATCGGCTTTTTCCTACGGCATAGTTCTGAC 575
531 CTATGACCTCAGCCCGCTGCTGCTGCGCCACCACTATATGCTATGCGCATGCTCTCAC 590
576 ATTGTCTGGCTTCT---TTCCCTCTCTTGGTCACTTTTGGTGTGCTATTCATGATGTCAG 633
591 TGTATCGGCTTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
634 GAGCTGATCAAGCCAGAGAGAACTCATGAGACAGGCAACACAGCCGCGGCGTGGCAAGGC 693
651 CCCTGCTGCGCAGGATGGCCGCGAGAGCTGTGGCCAGAGGGGGGGCTGGCAAGGC 710
694 CATCCGAGCATCTACTGTGTGTGGCTCTTACCCTCTGTTTGTGCTTGTGCTTGTGCTTGT 753
711 GGCCCGCATGGCGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
754 CATCGCTCTCTTACTCATCATCTGCTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTG 813
771 CACCAAGACAGCCTTACTTGGCAGTGGCTCGAGCCGCGGCTGCTGCTGCTGCTGCTGCTG 830
814 GGCAGCAGTGTGCTGCTTACAGATATGGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 873
831 GGCCTTGGAGCGGCTTACAAAGGCGCGGCTTGGCCAGGCGGCTTGGCCAGGCGGCTGCTG 890
874 CCCAGTCTCTACT 887
891 CCCATCTCTTCT 904

RESULT 10
US-08-513-974B-379
; Sequence 379, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1023 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..1020
; US-08-513-974B-379

Query Match 16.6%; Score 166.4; DB 3; Length 1023;
Best Local Similarity 52.1%; Pred. No. 1.1e-34;
Matches 445; Conservative 0; Mismatches 401; Indels 8; Gaps 3;

Qy 42 CTGCAGTTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTT 101
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 102 TATCTAGCGTGCACCTAAATGGCACTGTTGTGGCACTTCTGGGCCAAACCAAGCG 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 147 GCGGCTGGCTGGCGCTGAACATCTGTGTATTAACCAAGATCTCAAGTCCCGCGGCG 206
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 162 CTGGAGCTGTGCACCACTATCTGGTGAACCTGATGGTGGCGGACCTGCTTTATGTCT 221
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 207 CTTGACCCGACGCGCGGTACACCTTAACCTTGTCTGGCTGACCTGCTATATGCTG 266
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 222 AT---TGGCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTGGGGAGCT 278
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 267 CTCCCTGCCCCCTCATCTACAACATATGCCCAAGGTGATCACTGGCCCTTTGGCGACTT 326
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 279 GCTCTGCAAGTGGTGCCTTCTCTTATATCACTTTTACGGCAGCATCTGCTGCT 338
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 327 GCGCTGGCGCTGGTCCGCTTCTCTTATATGCCAACTTGACGCGAGCATCTTCTCT 386
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 339 GACCTGCATCTCTGTGCACCACTTCTTAGTGTGTGCCAACCCACCTGTGTGGCTGCCCTA 398
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 387 CACCTGCATCAGTTCACAGCGTACTTGGGCATCTGCCACCGCTGGCCCCCTGCGACAA 446
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

399 CC---GGACCGCAGGCGATGCTGGCTGGGCGACCGACACACCTGGGCGCTGGTGGCTCT 455
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
447 ACGTGGGGCGCGCGGCTGCTGGCTAGTGTGTAAACCGTGTGGCTGGCGGTGACAAAC 506
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
456 CCAGCTGCTGCCACACTGGCTTCTCCACACAGGACTACATCAATAGGCCAGATGATCTG 515
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
507 CCAGTGGCTGCCACAGCCATCTTGGCTGCGCACAGGATCCAGCGTAAACCGCACTGTCTG 566
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
516 GTATGACATGACGACCAAGAGATTTTGTATCGGCTTTTGGCTTACGGCATAGTCTGAC 575
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
567 CTATGACCTCAGCCCGCTGCCCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCAC 626
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
576 ATTGCTGGCTTTCT--TTCCCTCTCTTGGTCAATTTTGGTGTGCTATTCACTGATGGTCA 633
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
627 TGTCACTGGCTTCTGCTGCCCTTTGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
634 GAGCCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCGAGTGC 693
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
687 CCGCTGTGCGCGCAGGATGGCCCGGAGAGCCTGTGSCCCAGGAGCGGCTGGCAAGGC 746
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
694 CATCGGACCATCTACTGCTGGTGTGGCTTTTCACTCTGTTTGTGGCCCTTCCATAT 753
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
747 GCGCCGATGCGCGCTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
754 CACTCGCTCTTCTACCTCACCATCTGCTTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 813
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
807 CACCAAGACACCTTACCTGGCAGTGGCTGAGCGCGGGCGTCCCTGCACTGATATGGA 866
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
814 GGCAGCCAGTGTGGCTTACAGATATGAGAGCCCTCTGTGTAGTGTGAGCAGCTGCTCAA 873
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
867 GGCCTTTGCAGCGGCTTACAAAGGACGCGGCGCTTTGCCAGTGCCAAACAGCGTCTGA 926
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
874 CCCAGTCTGTACT 887
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
927 CCCCATCTCTTCT 940

RESULT 11
US-09-016-434-1108
; Sequence 1108, Application US/09016434
; Patent No. 650938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1108:
SEQUENCE CHARACTERISTICS:
LENGTH: 1571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1296659
US-09-016-434-1108

Query Match 15.4%; Score 164.8; DB 3; Length 1571;
Best Local Similarity 52.0%; Pred. No. 3.7e-34;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

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QY 42 CTGCCAGTTCTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101
DB 327 CTGTGTTACCGCGAGAACTTCAAGCAACTGCTCTGCCACCTGTGTATTCGGGGTGTCT 386
QY 102 TATCTTAGGGTGCCACTTAAGTGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
DB 387 GGCGGCTGGCTGCGCTGAACATCTGTGTCATTACCCAGATCTGCACGTCGCCCGCGGC 446
QY 162 CTGGAGCTGTGCCACCACTATCTGTGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCT 221
DB 447 CTTGACCCGCGACGCGCGCTGTACACCTTAACCTTTGCTCTGGCTGACCTGTATATGCTG 506
QY 222 AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
DB 507 CTCCTGCGCTGCTCATCTACAACTATGCCAAGTGATCACTGGCCCTTTGGCGACTT 566
QY 279 GCTCTGAAGTGCTGCACTTCTCTGTCTATATCAACCTTTACGGCAGCATCTCTGTGCT 338
DB 567 CGCTGCGCGCTGCTGCTGCTTCTTCTATGCAACCTTGCAAGGAGCATCTCTTCTTCT 626
QY 339 GACTGTGATCTGTGACCAAGTTCCTTAGTGTGTGCAACCACTGTGCTGCGCCCTA 398
DB 627 CACTGTGATCAGCTTCCAGCGCTACCTGGGCACTGCGCACCCGCTGGCCCTGGCAGAA 686
QY 399 CC---GGACCGCAGGATGCTGGCTGGGCAACCAACCACTGGCCCTGGTGTGCT 455
DB 687 ACGTGGGGCGCGCGCTGCTGGCTAGTGTGTAGCGGTGTGGCTGGCGGTGACAAC 746
QY 456 CCAGCTGCTGCCACACTGGCTTCTCCACAGCACTATCAATGGCCAGATGATCTG 515
DB 747 CCAGTGTCTGCCACAGCATCTTTCGCTGCGCACAGGCATCCAGCGTAACCGCACTGTCTG 806
QY 516 GTATGATGACGACGCAAGAAATTTTGTATCGGCTTTTGGCTTACGGCATAGTTCGAC 575
DB 807 CTATGACCTCAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTC 866
QY 576 ATTGCTGGCTTTCT---TTCCCTCTTGTGTCATTTTGTGCTGCTTACCTGATGTCAG 633
DB 867 TGTATCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 926
QY 634 GAGCTGTATCAAGCAGGAGGAACCTCATGAGGACAGGCAACACAGCCCGAGCAGGTC 693
DB 927 CCGCTGTGCGCGCAGGATGSCCGCGCAGAGCTGTGGCCAGGAGCGGTGCGCAAGGC 986
QY 694 CATCCGACCATCTACTGTGTGTGCTTTCACCTCTGTGTTTGTGCTTTCATAT 753
DB 987 GGCCCGCATGGCCGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
QY 754 CACTCGCTCTTCTACCTCACAATCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
DB 1047 CACCAAGACGCTTACTGGCAGTGCGCTGACGCGCGGGGTGCCCTGCACTGTATTTGA 1106
QY 814 GGCAGCAGTGTGCCCTTACAGATATAGAGCCCTCTGGTGTGTGTGTGTGTGTGTGTGTGT 873
DB 1107 GGCTTTTGACGCGCTTACAAAGGACACGCGCCGCTTTGCGCAAGTGCACAGCGGTGTGGA 1166
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QY 874 CCCAGTCTGTACT 887
DB 1167 CCCATCCTCTTCT 1180

RESULT 12
US-08-459-046-1
; Sequence 1, Application US/08459046
; Patent No. 6008039
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A No. 6008039el Human Purinergic P2U Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 Hillview Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,046
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0038 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Placenta
; CLONE: 179696
; US-08-459-046-1
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Query Match 15.8%; Score 158.4; DB 3; Length 984;
Best Local Similarity 51.5%; Pred. No. 1.6e-32;
Matches 440; Conservative 0; Mismatches 406; Indels 8; Gaps 3;

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QY 42 CTGCCAGTTCTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101
DB 51 CTGTGTTACCGGAGAACTTCAAGCAACTGTGCTCCCACTGTGTATTCGGGGTGTCT 110
QY 102 TATCTTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
DB 111 GGCGCTGCTCCCTCCGCTGAACATCTGTGTATTACCCAGATCTGCACGTCGCCCGCGGC 170
QY 162 CTGGAGCTGTGCCACCACTATCTGTGTGAACCTGTGTGGTGGCGGACCTGCTTTATGTGCT 221
DB 171 CTTGACCCGCGCGCGGTGTACACCTTAAACCTTTGCTCTGCTGACCTGTATATGCTG 230
QY 222 AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
DB 231 CTCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290
QY 279 GCTCTGCAAGCTGGTGCATCTTCTGTTTATATCAACCTTTACGGCAGCATCTCTGTGCT 338
DB 291 CGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
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QY 339 GACCTGCATCTCTGTGACACAGTTCTTAGGTGTGTGCCACCACTGTGTTGGCTGCCCTA 398
DB 111 GGCCTCTGCTCCGCTCGGTGAACATCTGTGTATTTACCAAGATCTGCAGTCCCGGGC 170
QY 162 CTGAGAGTGTGCCACCACTATCTGTGTGAACCTGATGGTGGCCAGCTGCTTTATGTGCT 221
DB 171 CCTGACCCGACGGCCGTGTACACCTAACTTGTCTGTGCTGACCTGCTATATGCTG 230
QY 222 AT---TGCCTCTCTCATCATCACTACTCATAGATGACAGGTGGCCCTTGGGGAGCT 278
DB 231 CTCCCTGCCCTGTCTCATCTACAATATGCCCAAGGTGATCATGTGGCCCTTTGGGAGCTT 290
QY 279 GCTCTGAAGCTGTGTCACCTTCTGTCTATATCAACCTTTACGGCAGCATCTCTGCTGCT 338
DB 291 CGCTTGGCGCTGTGCTGCTTCTCTTCTATGCAACCTTGCAACGGAGGATCTCTTCT 350
QY 339 GACCTGCATCTGTGACCAAGTTCTTAGGTGTGTGCCACCTGATGTTGCTGCTGCTGCTA 398
DB 351 CACCTGCATCAGCTTTCAGGCGCTACCTGGGCGATCTGCCACCCGCTGGCCCTTGCAAA 410
QY 399 CC---GGACCCGACAGCATGCTGCTGGGCAACCAAGCACTGCGGCCCTGGTGTCT 455
DB 411 ACCTGGGGCGCCGGGCTGCTGCTGTGTGTAGCCGTGTGGCTGGCGGTGACAAC 470
QY 456 CCAGCTGTGCCCACTGCTGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG 515
DB 471 CCAGTGCCTGCCCAAGCCATCTTGGCTGCCACAGGCATCCAGCGTAAACCCGACTGCTG 530
QY 516 GTATGACATGACCAAGCAAGAAATTTTGTGCTGCTTTTGTGCTAGCGCATGTTCTGAC 575
DB 531 TTATGACCTAGCCCGCTGCTGCTGGCCACCACTATATGCTTATGGATGGCTCTCAC 590
QY 576 ATTGTGCTGCTTCT--TTCCCTCTGTTGCTCATTTTGTGCTGCTATTCACATGATGCTG 633
DB 591 TGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
QY 634 GAGCTGATCAAGCAGAGGAGAACCTCATGAGGACAGGCAACAGCCCGGAGCGAGTGC 693
DB 651 CCGCTGTGCGCCAGGATGGCCGCGAGAGCTGTGGCCAGGAGCGGCTGGCAAGGC 710
QY 694 CATCCGACCATCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
DB 711 GGCCCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
QY 754 CACTGCTGCTTCTACTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813
DB 771 CACCAAGACAGCTTACCTGCGCTGCGCTCGAGCGCGGCGCTGCTGCTGCTGCTGCTGCT 830
QY 814 GCGAGCAGTGTGGCTTACAGATATGGAGGCGCTGCGCTGCGAGCGCGGCGCTGCGAGGC 873
DB 831 GGCCCTTTCAGCGGCTTACAAAGGACGCGCGCGTTCGCGAGTGCCACAGCGTGTGGA 890
QY 874 CCCAGTCTGCTACT 887
DB 891 CCCCATCTCTCTCT 904

RESULT 13

US-09-102-710B-1
; Sequence 1, Application US/09102710B
; Patent No. 6479630
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PF-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6479630 179696CB1
US-09-102-710B-1

Query Match 15.8%; Score 158.4; DB 3; Length 984;
Best Local Similarity 51.5%; Pred. No. 1.6e-32;
Matches 440; Conservative 0; Mismatches 406; Indels 8; Gaps 3;
QY 42 CTGCAGTTCTCAGAGAAGTCAAGCAAGTCTTACCTCTCCCTGGCCCTACAGTATCATTT 101
DB 51 CTGTGCTACCGCGAGAACTTCAAGCAACTGTGCTCCCACTGTGTATTGGGGGTGCT 110

QY 102 TATCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTTGGGGCCAAACCAAGCG 161
DB 111 GGCCTCTGCTCCGCTCGGTGAACATCTGTGTATTTACCAAGATCTGCAGTCCCGGGC 170
QY 162 CTGAGAGTGTGCCACCACTATCTGTGTGAACCTGATGGTGGCCAGCTGCTTTATGTGCT 221
DB 171 CCTGACCCGACGGCCGTGTACACCTAACTTGTCTGTGCTGACCTGCTATATGCTG 230
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QY 279 GCTCTGAAGCTGTGTCACCTTCTGTCTATATCAACCTTTACGGCAGCATCTCTGCTGCT 338
DB 291 CGCTTGGCGCTGTGCTGCTTCTCTTCTATGCAACCTTGCAACGGAGGATCTCTTCT 350
QY 339 GACCTGCATCTGTGACCAAGTTCTTAGGTGTGTGCCACCTGATGTTGCTGCTGCTGCTA 398
DB 351 CACCTGCATCAGCTTTCAGGCGCTACCTGGGCGATCTGCCACCCGCTGGCCCTTGCAAA 410
QY 399 CC---GGACCCGACAGGATGCTGCTGGGCGACCAAGCACTGCGGCCCTTGGTGTCT 455
DB 411 ACCTGGGGCGCCGGGCTGCTGCTGTGTGTGTAGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
QY 456 CCAGCTGTGCCCACTGCTGCTTCTCCACACAGGACTTACATCAATGGCCAGATGATCTG 515
DB 471 CCACTGCTGCCCAAGCCATCTTCTGCTGCCACAGGATCCAGCGTAAACCCGACTGCTG 530
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QY 576 ATTGTCTGCTTCT--TTCCCTCTTGTGCTATTTTGTGCTGCTTATTCACATGATGCTG 633
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QY 634 GAGCTGATCAAGCAGAGGAGAACCTCATGAGGACAGGCAACAGCCCGGAGCGAGTGC 693
DB 651 CCGCTGTGCGCCAGGATGGCCGCGAGAGCTGTGGCCAGGAGCGGCTGGCAAGGC 710
QY 694 CATCCGACCATCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753
DB 711 GGCCCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770
QY 754 CACTGCTGCTTCTACTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813
DB 771 CACCAAGACAGCTTACCTGCGCTGCGCTCGAGCGCGGCGCTGCTGCTGCTGCTGCTGCT 830
QY 814 GCGAGCAGTGTGGCTTACAGATATGGAGGCGCTGCGCTGCGAGCGCGGCGCTGCGAGGC 873
DB 831 GGCCCTTTCAGCGGCTTACAAAGGACGCGCGCGTTCGCGAGTGCCACAGCGTGTGGA 890
QY 874 CCCAGTCTGCTACT 887
DB 891 CCCCATCTCTCTCT 904

RESULT 14

US-08-513-974B-41
; Sequence 41, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

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STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-41

Query Match 15.0%; Score 150.4; DB 3; Length 984;
Best Local Similarity 50.9%; Pred. No. 2.2e-30;
Matches 435; Conservative 0; Mismatches 411; Indels 8; Gaps 3;

QY 42 CTGCAGTTCTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCCTACAGATATCATCTT 101
D 51 CTGCGTCTACCGTGAGGATTTCAAGCGACTGCTGCTAAACCCCGGTATATCTCGGTGGTCT 110
QY 102 TATCCTAGGCTGCCACTAAATGCACTGTCTTGTGGCACTTCTGGGGCCCAAAACGCG 161

STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
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PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-41

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162 CTGGAGCTGTGCCACCACCTATCTGTGTGAACCTGTGTGGCCGCACTGCTTTATGTGCT 221
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231 TTCACTACCCCTACTTTATCTATAAATACGCGCAGAGGGACCACTGGCCCTTCGGAGACCT 290
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339 GACTGTCATCTCTGTGCACCACTTCCTAGGTGTGTGCGCACCCACTGTGTTTCGCTGCCCTA 398
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399 CC---GGACCCGAGGATGCTGGCTGGGCACAGCACCACTGGGCCCTGGTGTGCT 455
411 GCGTGGAGGTGCGCGTGTGCTTGGGTAGTGTGGAGTGTGTGGCTGGCTGGCTGAGCAGC 470
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634 GAGCTGTATCAAGCCAGAGAGAGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
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694 CATCCGAGCATCTACTGTGTGTGGCTTTCACCCCTCTGTTTGTGTGCTTTCATAT 753
711 GGCTCGTATGGCTGTGTGTGGCAGCTGTCTTTTGGCATCAGCTTCTGCTTTCACAT 770
754 CACTGCTCTTCTACTCATCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 813
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814 GGCAGCCAGTGTGGCTTACAGATATGAGAGCCCTCTGGTGAGTGTGAGCAGCTGCCCAA 873
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874 CCGAGTCTGTACT 887
891 CCGCTTCTTCTCT 904

RESULT 15
US-09-461-436B-41
; Sequence 41, Application US/09461436B
; Patent No. 6538107
; GENERAL INFORMATION:
; APPLICANT: Shuji Hinuma
; Yasuaki Ito
; Ryo Fujii
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,
; Production, And Use Thereof
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edwards & Angell, LLP
; STREET: 101 Federal Street
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: PatentIn
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIORITY DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:

LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 41:

US-09-461-436B-41

Query Match i 15.0%; Score 150.4; DB 3; Length 984;
Best Local Similarity 50.9%; Pred. No. 2.2e-30;
Matches 435; Conservative 0; Mismatches 411; Indels 8; Gaps 3;
QY 42 CTGCCAGTTCTCAGAGAGTACAGCAAGTCTACTCTCCCTGGCTACAGTATCATCTT 101
DB 51 CTGGCTTACCGTGGAGGATTTCAAGCGACTGCTGCTAAACCCCGGTATCTCGGTGGTCT 110
QY 102 TATCTAGGGTGGCCACTAAATGGCACTGTCTTGGCACTCTGGGGCCAAACCAAGCG 161
DB 111 GGTGGTGGCGCTGCCACTGACATCTGGCTCATTTGCCAGATCTGGCATCCCGCGGAC 170
QY 162 CTGGAGCTGTGCCACCACTATCTGGTGAACCTGATGGTGGCCGACCTGCTTTATGGCT 221
DB 171 CCGTACCCGTTCCGCTGTGTACACCCCTGAACCTGGCACTGGCGGACCTGATGATGCGCTG 230
QY 222 AT---TGCCCTTCTCATCATCATCATCTACTACTGACAGGTGGCCCTTCGGGGAGCT 278
DB 231 TTCACTACCCCTACTTATCTATACTACGACAGGGGACCACTGGGCCCTTCGGAGACCT 290
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Search completed: February 15, 2006, 11:15:14
Job time : 227 secs

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QY 339 GACTGCTATCTCTGTGACACAGTTCTCTAGGTGTGTGCCACCACTGTGTTGCTGCCCCTA 398
Db 351 CACCTGCATTAGCTTTCAGCGCTTACCTGGGCACTGTGCCACCCCTGGCTTCTTGCCACAA 410
QY 399 CC---GGACCCGCGAGGATGCTGCTGGTGGGCAACAGACACCACTGGGGCCCTGGTGGTCT 455
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QY 456 CCAGCTGCTGCCACACTGCGCTTCTCCCAACAGGACTATCAATGAGCCAGAGATGATCTG 515
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QY 576 ATTGCTGGCT--TTCTTTCCCTCTTGGTCAATTTGGTGTGCTATTCACTGATGGTCTCAG 633
Db 591 GGTCACTGGCTTCTTGTGCTTCCCTTCATAGCCTTACTGGCTTGTATTGTGCAATGGCCCG 650
QY 634 GAGCCTGATCAAGCCAGAGGAGAACTCTATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
Db 651 CCGCTGTGTGCGCAGGATGGCCCGCAGAGGTCTCTGTGGCCCAAGAGCGGCGCAGCAAGGC 710
QY 694 CATCGGACCATCTACTGTGTGGCTTTCACCCCTCTGTTTGTGGCCCTTCCATAT 753
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QY 754 CACTCGCTCTTCTACCTCACCATCTGCTTTCTGCTTCTCAGGACTGCCAGCTCTTGAT 813
Db 771 CACCAAGACAGCTTACTTGGCTGCGCTCACCGCGGTGTCTCTTGGCTGTGCTGA 830
QY 814 GGCAGCCAGTGTGGCTTACAGATATGAGAGCCCTCTGTGTAGTGTGAGCAGCTGCTCAA 873
Db 831 GACCTTGGCTGCTGCTACAAAGGCACTCGGCCCTTGGCCAGTGTCAACAGTGTCTGGA 890
QY 874 CCCAGTCTGTACT 887
Db 891 CCCAATCTCTTCT 904

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:38:34 ; Search time 40 seconds
(without alignments)
801.005 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	379	20.9	373	2	A47556
5	375	20.7	365	2	S68679
6	354	19.5	362	2	S33733
7	336	18.5	373	2	JC4737
8	334.5	18.5	373	2	JC4162
9	280.5	16.0	308	2	I50241
10	282.5	15.6	344	2	T09508
11	263.5	14.5	370	2	JC5549
12	259.5	14.3	353	2	JC2492
13	254	14.0	399	2	I48705
14	249.5	13.8	359	2	S15403
15	246.5	13.6	359	2	S44425
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23	239	13.2	359	2	JC2134
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26	235.5	13.0	391	2	C41795
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29	232.5	12.8	423	2	JC7677

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31 231.5 12.8 362 2 S68207 G protein-coupled
32 231.5 12.8 362 2 A57641 G protein-coupled
33 231 12.7 360 2 JC4587 chemokine (C-C) re
34 228.5 12.6 359 2 JQ1516 angiotensin II rec
35 227.5 12.6 362 2 B57641 G protein-coupled
36 227 12.5 352 1 S27357 complement C5a ana
37 226 12.5 372 2 S26667 G protein-coupled
38 225.5 12.4 380 2 I38435 angiotensin recept
39 225.5 12.4 427 2 S17148 alpha-thrombin rec
40 224 12.4 371 2 JC5498 G protein-coupled
41 222 12.3 398 2 I56504 mu opioid receptor
42 221.5 12.2 333 2 I65989 G protein-coupled
43 221.5 12.2 359 2 I51372 angiotensin II rec
44 221 12.2 398 2 A57510 mu opioid receptor
45 221 12.2 398 2 I56517 mu opioid receptor

ALIGNMENTS

RESULT 1

I55450

G protein-coupled P2 receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I55450

R:Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.

J. Biol. Chem. 270, 26152-26158, 1995

A:Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.

A:Reference number: I55450; MUID:96064682; PMID:7592819

A:Accession: I55450

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <RES>

A:Cross-references: UNIPROT:Q63371; UNIPARC:UPI0000131003; GB:D63665; NID:G1066007; PIDIN

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor

Query Match 22.2%; Score 402; DB 2; Length 328;

Best Local Similarity 32.5%; Pred. No. 2.8e-27;

Matches 108; Conservative 53; Mismatches 137; Indels 34; Gaps 9;

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Qy	57	CATTYLVNLMVADLLYYVL-LPFLIITYSLDDRWPFGBELLCKLVHFLFYINLYGSILLTC 115
Db	60	RSAYVTNLALADLLYACSLPLLIYNYARGDHPFGLACRLVRFVFLVYANLHGSILFLTC 119
Qy	116	ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTWALVVLQLLPTLAFSHTDYINGOMIWD 174
Db	120	ISFORYLIGICHPLAPMWHKRGGRRAAVVGVVVLVVTAAQCLPTAVFAATGQRNRTVCD 179
Qy	175	MTSQENFDRLFAYGIVLTLSGLF---SLLGHFGLFTDQGPQARCEPHEDRHSFSQ 230
Db	180	LSPPIILSTRILPYGMALTVIGFLPFTALLACYCRMARRLCRQDGPAGVQAERSKAAR 239
Qy	231	VHPDHPGTGVNPLFCALPYHSLLLPHLL-SAFSGLPALDGSQCGLQDMSEACEBQL 289
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Qy	290	PQPS-----PVLSF-----KGGKNRVRLLQKL 311
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RESULT 2

JC4800

P2Y6 receptor - human

C:Species: Homo sapiens (man)

C:Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

QY 194 SGFLSLGHFGVLF-----TDGQEPDQGEPRHEDRO--HSPSOV 231
DB 203 ---IGLL--FAVPFVILVCYVLMARRLLKPAYGTG-----GLPRAKRSVETIALV 250
QY 232 HPDHTGVMPLHPLFCALPYH-----SLLLPHLLSAFS-----GLPALDGSQCG 276
DB 251 ----LAVFAL----CFLPFHVRTLYYSFRSLDLSCHTLNAINMAYKITRPLASANS- 300
QY 277 LQDMEASGECEQLPOPSVLSFKGKNRVLLQKLR-----QNKLGHEHPAGR 323
DB 301 -----LDPVLYFLAQQLRVRFARDAKPTEPTPSQARRKGLGHRPNR 343

RESULT 5
S86679
G protein-coupled receptor - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68679
R:Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett. 384, 260-264, 1996
A:Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expressed in rat liver
A:Reference number: S68679; MUID:96197801; PMID:8617367
A:Accession: S68679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STA>
A:Cross-references: UNIPROT:P51582; UNIPARC:UPI000002E776; EMBL:X96597; NID:g1296631; PDB:1YUW
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor

Query Match 20.7%; Score 375; DB 2; Length 365;
Best Local Similarity 41.7%; Pred. No. 6.9e-25;
Matches 80; Conservative 30; Mismatches 74; Indels 8; Gaps 3;

QY 15 CQFSKYQVYLSLAYSIIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLVYL 74
DB 27 CWFDEDFKILLPVSYAVVFLGLGNAPTLWLFIFRLRPWDATATYMFHLASTLTVL 86

QY 75 -LPFLIIITYSLDDRWPFGECLLKVHFLFYINLYSGIILLTTCISVHQFLGVCHPLCSLPY 133
DB 87 SLPTLIYYAAHNHPFPGTEICKFVRFLFYNNLYCSVLFLTTCISVHRVLYGICHPLRALRW 146

QY 134 RTRRHAWLGTSTWALVQLLPTLAFSHDTYINGQMIWYDMSQENPDRLFAVGIVLTL 193
DB 147 GRPLRAGLCLAVLWLVAGCLVPLNFVFTTSNKGTTVLCHDTRPEEFDHYVHFS----- 201

QY 194 SGFLSLGHFGV 205
DB 202 SAVMGLL--FGV 211

RESULT 6
S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33733
R:Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FEBS Lett. 324, 219-225, 1993
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A:Reference number: S33733; MUID:93285340; PMID:8508924
A:Accession: S33733
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <WEB>
A:Cross-references: UNIPROT:P34996; UNIPARC:UPI00000405D4; EMBL:X73268; NID:g395084; PDB:1YUW
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.5%; Score 354; DB 2; Length 362;
Best Local Similarity 30.8%; Pred. No. 4.5e-23;
Matches 98; Conservative 49; Mismatches 127; Indels 44; Gaps 10;

QY 25 YLSLAYSIIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLVYL-LPFLIIITYS 83
DB 42 YLPTVYIIIVFITFGIGNSVAIWVFHMRPWSGIVSYMFNLALADFLVTLTPALIFYFYF 101

QY 84 LDDRWPFGELCKLVHFLFYINLYSGIILLTTCISVHQFLGVCHPLCSLPYRTRHAWLGT 143
DB 102 NKTDWIFGDVCKLQRFIFHVNLYGSILFLTTCISVHRVYGVVHPLKSLGRLLKKNVYVS 161

QY 144 STTWALVQLLPTLAFSHDTYINGQMI-WYDMSQENPDRLFAVGIVLTL-----SGFLS 198
DB 162 SLVWALVAVIAPILFYSGTVRRNKTTITCYDTTADAYLSRVFYVSMCTTVFMFCIPFTV 221

QY 199 ILGHFGVLFDTGQEPDQGEPRHEDROHSPSOVHDPHTGVWPLHPLFCALPVHSL-LLP 257
DB 222 ILGCYGLI-----VKALIYKDLNDSPLRRK-----SIYLVIIIVLTVFAVSYP 264

QY 258 HHLISAFSGLPALD---GSQCGLOD-----MEASGECEQLPOPSVLSFKGKN 303
DB 265 FHVMTLNLRARLDFTQPMCAFNDKVATYQVTRGLASLNSC-----VDPILYFLAGDT 319

QY 304 -RVRLQLKLRQNKLGHEHP 320
DB 320 FRRRLSRATKSSRRSEP 337

RESULT 7
JC4737
G protein-coupled receptor P2Y1 - human
N:Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4737; JC4615; S54253
R:Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A:Title: Cloning and tissue distribution of the human P2Y1 receptor.
A:Reference number: JC4737; MUID:96205320; PMID:8630005
A:Accession: JC4737
A:Molecule type: DNA
A:Residues: 1-373 <JAN>
A:Cross-references: UNIPROT:P47900; UNIPARC:UPI0000001C06; GB:S81950; NID:g1839438; PDB:1YUW
R:Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Achwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A:Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A:Reference number: JC4615; MUID:96158962; PMID:8579591
A:Accession: JC4615
A:Molecule type: mRNA
A:Residues: 1-373 <AYY>
A:Cross-references: UNIPARC:UPI0000001C06; GB:U42029; NID:g1147730; PIDN:AAA97872.1; PFI
A:Experimental source: erythro leukemia cells
R:Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
Submitted to the EMBL Data Library, May 1995
A:Description: Cloning of a human putative P2Y receptor.
A:Reference number: S54253
A:Accession: S54253
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137,139-373 <LEO>
A:Cross-references: UNIPARC:UPI000016A5B9; EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PFI
C:Comment: This receptor belongs to a family of G protein-coupled receptors. It respond
C:Genetics:
A:Gene: P2Y1; GDB:P2RY1
A:Cross-references: GDB:677125; OMIM:601167
A:Map position: 3pter-3qter
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:52-77/Domain: transmembrane #status predicted <TML>
F:88-111/Domain: transmembrane #status predicted <TM2>
F:124-152/Domain: transmembrane #status predicted <TM3>
F:171-191/Domain: transmembrane #status predicted <TM4>
F:214-237/Domain: transmembrane #status predicted <TM5>
F:261-282/Domain: transmembrane #status predicted <TM6>
F:305-328/Domain: transmembrane #status predicted <TM7>

N:Alternate names: G-protein coupled receptor

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T09508

R:Bohm, S.K.; Trumpff, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.

submitted to the EMBL Data Library, April 1997

A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob

A:Reference number: Z16705

A:Accession: T09508

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-344 <BO>

A:Cross-references: UNIPROT:P43657; UNIPARC:UPI000005041B; EMBL:AF000546; NID:g2232068;

C:Genetics:

A:Map position: 13

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.6%; Score 282.5; DB 2; Length 344;

Best Local Similarity 34.3%; Pred. No. 6.8e-17;

Matches 71; Conservative 39; Mismatches 76; Indels 21; Gaps 7;

QY 4 VDMNTSQBGLQCFSEKQKVYLSAYSIIFILGLPLNGTVMWHFWGQTKRWSCATTYLV 63

Db 2 VSVNSH---CFYNDSPKTYLGYCMFSVFLGLVSNCAIYIFICVLKVRNETTYMI 57

QY 64 NLWVADLLVYL-LPFLIITYSLDDRWPGELLCKLVHFLFYINLYGSILLITCISVHQPL 122

Db 58 NLAMSDLLFVFTLPPRIIF-YFTTRNWPFGDLLCKISVMFLFTNYMYSILFLTCISVDRL 116

QY 123 GVCHPLCSLPYRTRRHAWLGSTTWALVVLQLLPT--LAFSHTDYINGQMIWYDNTSEN 180

Db 117 AIYVFPKSKTLTKKNAKIVCTGWLTVIGSAPAVFQSTHSQGNASEACF-----EN 171

QY 181 FD----RLFAYGIVLTSLGFLSLGLGHF 203

Db 172 PPEATWKTYLSRIVI----FIEIVGFF 194

RESULT 11

heptahelical P2Y5-like receptor - human

C:Species: Homo sapiens (man)

C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004

C:Accession: JC5549

R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.

Biochem. Biophys. Res. Commun. 236, 106-112, 1997

A>Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.

A:Reference number: JC5549; MUID:97366605; PMID:9223435

A:Accession: JC5549

A:Molecule type: DNA

A:Residues: 1-370 <JAN>

A:Cross-references: UNIPROT:Q99677; UNIPARC:UPI000016A4CA; DBJ:AF005419; NID:g2240034;

C:Superfamily: ATP receptor P2u

Query Match 14.5%; Score 263.5; DB 2; Length 370;

Best Local Similarity 34.0%; Pred. No. 3.3e-15;

Matches 69; Conservative 34; Mismatches 89; Indels 11; Gaps 4;

QY 5 DMNTSQEQL-----CFSEKQKVYLSAYSIIFILGLPLNGTVMWHFWGQTKRWS 56

Db 13 DSNLSRLPRLGNATANTTCIVDDSPKYNLNGAVSVVFLGLITNSVLSLFCFPMKWS 72

QY 57 CATTYLVNLMVADLLVYL-LPFLIITYSLDDRWPGELLCKLVHFLFYINLYGSILLITC 115

Db 73 ETAIFITNLAVSDLLFVCTLPKIF-YNPNRHWPFQDYLCKISGTAFLTNYGSMFLFTC 131

QY 116 ISVHQLFVCHPLCSLPYRTRRHAWLGSTTWALVVLQLLPTLAFSHTDYINGQMIWYD 175

Db 132 ISVDRLFAIVYFPRGRTTRNSAIVCAVGWILVLSGISASLSFTTNVNNATTCTCEG 191

QY 176 TSQENFDR-LPAYGVLTSLGFL 197

Db 192 LSKRVWKTYLSKITIFIEVVGFI 214

RESULT 12

JC2492

G protein-coupled receptor 1 - rat

N:Alternate names: GPR-1

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C:Accession: JC2492

R:Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.R.

Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994

A>Title: Mapping studies of two G protein-coupled receptor genes: An amino acid differen

A:Reference number: JC2492; MUID:95110347; PMID:7811287

A:Accession: JC2492

A:Molecule type: mRNA

A:Residues: 1-353 <MAR>

A:Cross-references: UNIPROT:P46090; UNIPARC:UPI000012BA30; GB:S74702; NID:g786483; PIDN:

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transmem

F:74-94/Domain: transmembrane #status predicted <TM2>

F:112-133/Domain: transmembrane #status predicted <TM3>

F:134-135/Region: DR motif

F:155-175/Domain: transmembrane #status predicted <TM4>

F:209-229/Domain: transmembrane #status predicted <TM5>

F:246-266/Domain: transmembrane #status predicted <TM6>

F:295-306/Domain: transmembrane #status predicted <TM7>

F:14,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict

F:330/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 14.3%; Score 259.5; DB 2; Length 353;

Best Local Similarity 33.3%; Pred. No. 6.9e-15;

Matches 64; Conservative 35; Mismatches 68; Indels 25; Gaps 5;

QY 28 LAYSIIFILGLPLNGTVMWHFWGQTKRWSCATTYLVNLMVADLLVYL-LPFLIITYSLDD 86

Db 43 LLYALAVILGIPGNAIVIV-FMGFKWKKTVTTLWFLNLAIADFIPLFLPLVYSVALSF 101

QY 87 RWPFGELLCKLVHFLFYINLYGSILLITCISVHQLFVCHPLCSLPYRTRRHAWLGSTTT 146

Db 102 HWPFGRLCKLNSFIAQLNMFSSVFFLTVISLDRIYIHLHPGLSHPHRTLKNSLLVLFV 161

QY 147 WALVVLQLLPTLAFSHTDYINGQMIWYDNTSQENFDRL-----FAYGIVLT 192

Db 162 WLLASLLGGPPLYPRDTVEVNNRIICYN-----NFQSYELTMRHHVLTWVKFLFGYLLP 216

QY 193 L-----SGFLSL 200

Db 217 LLTWSVCYLCL 228

RESULT 13

148705

proteinase activated receptor 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48705

R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.

J. Biol. Chem. 270, 5950-5955, 1995

A>Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and

A:Reference number: I48705; MUID:95197620; PMID:7890726

A:Accession: I48705

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-399 <RBS>

A:Cross-references: UNIPROT:P55086; UNIPARC:UPI0000021CA2; EMBL:Z48043; NID:g663020; PID

C:Superfamily: ATP receptor P2u

Query Match 14.0%; Score 254; DB 2; Length 399;

Best Local Similarity 35.6%; Pred. No. 2.4e-14;

Matches 69; Conservative 34; Mismatches 79; Indels 12; Gaps 7;

```

QY 20 KYKOVLSLAYSIIIFILGLPLNGTVLWHEWQTKRWSGATTVLNLVADLLVLLPPLI 79
Db 74 KLTVFLPVVYIIIVFVIGLPSNGMALWIFRTKKKHPAVIYMANLADLLSVWPPKL 133
QY 80 ITYSL-DRWPFGELLCVHLFVYINLYSILLTTCISVHQFVGCVCHPLCSLPYRTRH 138
Db 134 ISYHLGNWVYVYGCALCKVLGFFYGNMYCSILFWTCLSVQRYWVIVNPM-GHP-RKAN 191
QY 139 AWLQTS-TTVALVQLLPTLAFSHDYINGQMI--WYDMSQBNF-DRLPAYGIVLTLS 194
Db 192 IAVGSLAIWLLIFLWVQTIIPALNITTCHDVLPEBVLGDMFNFLSLAIG 251
QY 195 GFLSLGHFGVLFT 208
Db 252 VFL-----FPALLT 260

RESULT 14
S15403
angiotensin II receptor type 1 - bovine
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S15403
R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Mateuda, Y.
Nature 351, 230-233, 1991
A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angioten
A:Reference number: S15403; MUID:91251900; PMID:2041569
A:Accession: S15403
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: UNIPARC:UPI000012568B; GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
C:Superfamily: vertebrate rhodopsin

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Query Match 13.8%; Score 249.5; DB 2; Length 359;
Best Local Similarity 31.0%; Pred. No. 5.2e-14;
Matches 63; Conservative 42; Mismatches 87; Indels 11; Gaps 4;

QY 6 MNTSQEQL-----QCFSEKYKQVYLSL--AYSIIIFILGLPLNGTVLWHEWQTKRWSG 57
Db 3 LNSSTEDGIRIQQDCPKAGRHNVIIFVIMPTLSIIIFVVGIFGNSLVVIVYFYMKLKV 62
QY 58 ATTLYNLVADLLVYL-LPFLIITYSLDDRWPFGBELCKLVHFLFYINLYGSLILLTCI 116
Db 63 ASVFLNLALADLCFLTLPLWAVYTAMEYRWPFGNVLCKIASASVSFNLYASVFLLTCL 122
QY 117 SVHQFLGCVCHPLCSLPYRTRRHAWLGTSTTWALVQLLPTLAFSHDYINGQMIWYDMT 176
Db 123 SIDRYLAIVHPMKSRRLRTMLVAKVTCIIIWLLAGLASLPTIIHRNVFFIENTNITVCAF 182
QY 177 SQENFDRLFAYGIVLT--LSGFL 197
Db 183 HYESQNSTLPVGLGLTKNILGFL 205

```

```

RESULT 15
S44425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor w
A:Reference number: S44425; MUID:94222188; PMID:8168620
A:Accession: S44425
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <BUR>
A:Cross-references: UNIPROT:P43240; UNIPARC:UPI000012568C; PIDN:AAB30674.1; PID:g546569
A:Experimental source: liver
C:Superfamily: vertebrate rhodopsin

```

```

Query Match 13.6%; Score 246.5; DB 2; Length 359;
Best Local Similarity 30.5%; Pred. No. 9.5e-14;
Matches 62; Conservative 43; Mismatches 87; Indels 11; Gaps 4;

QY 6 MNTSQEQL-----QCFSEKYKQVYLSL--AYSIIIFILGLPLNGTVLWHEWQTKRWSG 57
Db 3 LNSSTEDGIRIQQDCPKAGRHNVIIFVIMPTLSIIIFVVGIFGNSLVVIVYFYMKLKV 62
QY 58 ATTLYNLVADLLVYL-LPFLIITYSLDDRWPFGBELCKLVHFLFYINLYGSLILLTCI 116
Db 63 ASVFLNLALADLCFLTLPLWAVYTAMEYRWPFGNVLCKIASASVSFNLYASVFLLTCL 122
QY 117 SVHQFLGCVCHPLCSLPYRTRRHAWLGTSTTWALVQLLPTLAFSHDYINGQMIWYDMT 176
Db 123 SIDRYLAIVHPMKSPVRRRTMLMAKVTCIIIWLLAGLASLPTIIHRNVFFIENTNITVCAF 182
QY 177 SQENFDRLFAYGIVLT--LSGFL 197
Db 183 HYESQNSTLPVGLGLTKNILGFL 205

```

Search completed: February 13, 2006, 14:43:02
Job time : 41 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 14:35:44 ; Search time 232 Seconds
(without alignments)
1012.676 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

Sequence: 1 MEKVDNMTSQBGLQCFSEK.....NKLGEHPAGRKRCPLNRSG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	99.6	361	2 Q711G2 HUMAN	Q711G2 homo sapien
2	449	24.8	328	1 P2RY3 CHICK	O98907 gallus gall
3	449	24.8	328	1 P2RY3 MELGA	O93361 meleagris g
4	429	23.7	374	2 O57466 MELGA	O57466 meleagris g
5	424	23.4	537	1 P2RY8 XENLA	P79928 xenopus lae
6	422	23.3	537	2 Q7ZM07 XENLA	Q7ZM07 xenopus lae
7	420.5	23.2	310	2 Q4SEL5 TETNG	Q4sel5 tetraodon n
8	411	22.7	543	2 Q5BJ79 XENTR	O5bj79 xenopus tro
9	405.5	22.4	308	2 Q4SEL9 TETNG	Q4sel9 tetraodon n
10	402	22.2	328	1 P2RY6 RAT	Q63371 rattus norv
11	397	21.9	328	1 P2RY6 MOUSE	Q98rk9 mus musculu
12	396	21.9	361	1 P2RY4 RAT	O35811 rattus norv
13	395.5	21.8	328	2 Q5R5L5 PONPY	O5r5l6 pongo pygma
14	395.5	21.8	377	1 P2RY2 HUMAN	P41231 homo sapien
15	394	21.7	361	1 P2RY4 MOUSE	Q9jj87 mus musculu
16	389.5	21.5	328	1 P2RY6 HUMAN	Q15077 homo sapien
17	389.5	21.5	347	2 Q7Z2A4 BRARE	Q7zza4 brachydanio
18	383.5	21.2	373	2 Q5YA25 PIG	O5ya25 sus scrofa
19	379	20.9	373	1 P2RY2 MOUSE	P53383 mus musculu
20	378	20.9	365	2 Q4VBB8 HUMAN	Q4vbb8 homo sapien
21	376.5	20.8	302	2 Q4RP73 TETNG	Q4rp73 tetraodon n
22	375	20.7	365	1 P2RY4 HUMAN	P51582 homo sapien
23	375	20.7	365	2 Q502W2 HUMAN	Q502w2 homo sapien
24	375	20.7	365	2 Q4VBB7 HUMAN	Q4vbb7 homo sapien
25	375	20.7	365	2 Q5JT22 HUMAN	Q5jt22 homo sapien
26	374.5	20.7	374	1 P2RY2 RAT	P41232 rattus norv
27	371.5	20.5	349	2 Q6P852 XENTR	Q6p852 xenopus tro
28	367	20.3	357	2 Q9DE05 RAJER	Q9de05 raja erinac
29	367	20.3	358	2 Q4SPQ4 TETNG	Q4spq4 tetraodon n
30	365	20.1	230	2 Q5Y809 PIG	O5y809 sus scrofa
31	354	19.5	362	1 P2RY1 CHICK	P34996 gallus gall

32	354	19.5	362	1 P2RY1 MELGA	P49652 meleagris g
33	339	18.7	182	2 Q5DKX2 PIG	O5dkx2 sus scrofa
34	337.5	18.6	361	2 Q90X57 XENLA	O90x57 xenopus lae
35	337.5	18.6	373	1 P2RY1 CAVPO	P59902 cavia porce
36	337.5	18.6	373	1 P2RY1 RAT	P49651 rattus norv
37	336	18.5	373	1 P2RY1 HUMAN	P47900 homo sapien
38	335.5	18.5	268	2 Q5DKX3 PIG	Q5dkx3 sus scrofa
39	334.5	18.5	373	1 P2RY1 BOVIN	P48042 bos taurus
40	328	18.1	373	1 P2RY1 MOUSE	P49650 mus musculu
41	328	18.1	373	2 Q544J5 MOUSE	Q544j5 m adult mal
42	325.5	18.0	373	2 Q5XX73 CANFA	Q5xx73 canis famli
43	325	17.9	373	2 Q8BMJ5 MOUSE	Q8bmj5 mus musculu
44	290.5	16.0	302	2 Q4S8W3 TETNG	Q4s8w3 tetraodon n
45	290.5	16.0	308	1 P2RY5 CHICK	P32250 gallus gall

ALIGNMENTS

RESULT 1
Q711G2 HUMAN
ID Q711G2 HUMAN PRELIMINARY; PRT; 361 AA.
AC Q711G2;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Nucleoside/nucleotide receptor.
GN Name=P2Y2-like;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Bruss M., Bonisch H., Kugelgen I.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Bruess M.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ345013; CAC87811.1; -, Genomic DNA.
DR GO; GO:0016021; C:integral to membrane, IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR GO; GO:0004872; F:purinergic activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR002286; P2_purinocptor.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PRINTS; PR00453; VWFADOMAIN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 361 AA; 40633 MW; 3992A1A1EF512AFE CRC64;

Query Match 99.6%; Score 1804; DB 2; Length 361;
Best Local Similarity 99.7%; Pred. No. 4.7e-125;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MEKVDNMTSQBGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60
DB	29	MEKVDNMTSQBGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88
QY	61	YLNLNMLVADLLYVLLPFLIIITYSLDDRPFFGELLCKLVHFLFYINLYGSIILLTTCISVHQ 120
DB	89	YLNLNMLVADLLYVLLPFLIIITYSLDDRPFFGELLCKLVHFLFYINLYGSIILLTTCISVHQ 148
QY	121	FLGVCHPLCSPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDWTQSBN 180

```
Db 149 FLGVCHFLCSFYRIRHAWLGSTTTWALVVLQPLTAFSHTDYINGQMIWDMTSQEN 208
Qy 181 FDLRFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPHEHQHSPQVHPDHPGTGV 240
Db 209 FDLRFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPHEHQHSPQVHPDHPGTGV 268
Qy 241 PLHLFLCPLPYSLLLPHLLLSAFSGLPALDGSQGLQDMEASGECQLPQPSVLSPFKG 300
Db 269 PLHLFLCPLPYSLLLPHLLLSAFSGLPALDGSQGLQDMEASGECQLPQPSVLSPFKG 328
Qy 301 GKNNRVLLOKLQRQNKLGEPHAGRCPCPLNRSG 333
Db 329 GKNNRVLLOKLQRQNKLGEPHAGRCPCPLNRSG 361

RESULT 2
P2RY3_CHICK
ID P2RY3_CHICK STANDARD; PRT; 328 AA.
AC Q98907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN Name=P2RY3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Webb T.E., Henderson D., King B.F., Wang S., Simon J., Bateson A.N.,
RA Burnstock G., Barnard E.A.;
RT "A novel G protein-coupled P2 purinoceptor (P2Y3) activated
RT preferentially by nucleoside diphosphates.";
RL Mol. Pharmacol. 50:258-265(1996).
CC -!- FUNCTION: Receptor for extracellular ADP > UTP = UDP. The
CC activity of this receptor is mediated by G proteins which activate
CC a phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X98283; CAA66930.1; -; mRNA.
CC HSP; P34996; 1DDDD.
CC Ensembl; ENSGALG0000017327; Gallus gallus.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR002286; P2_purnocptor.
CC InterPro; IPR000371; P2Y3_purnocptor.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01065; P2YPURNOCPTR.
CC PRINTS; PR01157; P2YPURNOCPTR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; GPCPROTEIN; Receptor; Transducer;
CC Transmembrane.
Kw TOPO_DOM 1 22 Extracellular (Potential).
Kw TRANSMEM 23 43 1 (Potential).
Kw TRANSMEM 44 57 Cytoplasmic (Potential).
Kw TOPO_DOM 58 78 2 (Potential).
Kw TRANSMEM 79 96 Extracellular (Potential).
Kw TRANSMEM 97 117 3 (Potential).
Kw TOPO_DOM 118 139 Cytoplasmic (Potential).
Kw TRANSMEM 140 160 4 (Potential).
Kw -----
```

```
FT TOPO_DOM 161 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 231 Cytoplasmic (Potential).
FT TRANSMEM 232 252 6 (Potential).
FT TOPO_DOM 253 275 Extracellular (Potential).
FT TRANSMEM 276 298 7 (Potential).
FT TOPO_DOM 299 323 Extracellular (Potential).
FT CARBOHYD 5 5 N-linked (GlcNAc..) (Potential).
FT DISULFID 94 172 By similarity.
SQ SEQUENCE 328 AA; 37587 MW; 7A3BF1C91F54FAAB CRC64;

Query Match 24.8%; Score 449; DB 1; Length 328;
Best Local Similarity 45.9%; Pred No. 4.3e-25;
Matches 85; Conservative 31; Mismatches 67; Indels 2; Gaps 2;

Qy 15 CQFSEKQVYLSLAYSIIFILGLPLNGTVLMHFWGQTKRWSCATTYVNLAMVADLLYL 74
Db 13 CTFHEBFQVLLPLVYSVVFLLGLPLNAVVGQIWLARKALTRTTIYMLNLAMADLLYVC 72
Qy 75 -LPFLIITYSLDDRWPFGELLCKLVHPLFYINLYGSIILLITCSVHQFLGVCHPLCSL-P 132
Db 73 SLPELLIYNTQKDYWPFQDFTCKFVFQFYTNLHGSILFLTCSVQRYMGICHPLASWHK 132
Qy 133 YRTRRHAWLGSTTTWALVVLQPLTAFSHTDYINGQMIWDMTSQENFDRLFAYGIVLT 192
Db 133 KKQKLTWLVCAAVFIVIAQCLPTFVFASGTQRNRTVCYDLSPDPDRSTSYPPYGITLT 192
Qy 193 LSGFL 197
Db 193 ITGFL 197

RESULT 3
P2RY3_MELGA
ID P2RY3_MELGA STANDARD; PRT; 328 AA.
AC O93361;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN Name=P2RY3;
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Li Q., Oleesky M., Palmer R.K., Harden T.K., Nicholas R.A.;
RT "Evidence that the p2y3 receptor is the avian homologue of the
RT mammalian P2Y6 receptor.";
RL Mol. Pharmacol. 54:541-546(1998).
CC -!- FUNCTION: Receptor for extracellular UDP > ADP = UTP. The activity
CC of this receptor is mediated by G proteins which activate a
CC phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF069555; AAC23863.1; -; Genomic_DNA.
CC HSP; P34996; 1DDDD.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR002286; P2_purnocptor.
CC InterPro; IPR000371; P2Y3_purnocptor.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01065; P2YPURNOCPTR.
CC PRINTS; PR01157; P2YPURNOCPTR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; GPCPROTEIN; Receptor; Transducer;
CC Transmembrane.
Kw TOPO_DOM 1 22 Extracellular (Potential).
Kw TRANSMEM 23 43 1 (Potential).
Kw TRANSMEM 44 57 Cytoplasmic (Potential).
Kw TOPO_DOM 58 78 2 (Potential).
Kw TRANSMEM 79 96 Extracellular (Potential).
Kw TRANSMEM 97 117 3 (Potential).
Kw TOPO_DOM 118 139 Cytoplasmic (Potential).
Kw TRANSMEM 140 160 4 (Potential).
Kw -----
```



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DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01066; P2Y4RNOCPTR.
DR PRINTS; PR01157; P2Y4RNOCPTR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 49 Extracellular (Potential).
FT TRANSHEM 50 70 1 (Potential).
FT TOPO_DOM 71 79 Cytoplasmic (Potential).
FT TRANSHEM 80 100 2 (Potential).
FT TOPO_DOM 101 118 Extracellular (Potential).
FT TRANSHEM 119 139 3 (Potential).
FT TOPO_DOM 140 161 Cytoplasmic (Potential).
FT TRANSHEM 162 182 4 (Potential).
FT TOPO_DOM 183 210 Extracellular (Potential).
FT TRANSHEM 211 231 5 (Potential).
FT TOPO_DOM 232 254 Cytoplasmic (Potential).
FT TRANSHEM 255 275 6 (Potential).
FT TOPO_DOM 276 292 Extracellular (Potential).
FT TRANSHEM 293 316 7 (Potential).
FT TOPO_DOM 317 537 Cytoplasmic (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 29 29 N-linked (GlcNAc...) (Potential).
FT DISULFID 116 193 By similarity.
SQ SEQUENCE 537 AA; 62024 MW; B2CF24812F3C19F2 CRC64;

Query Match 23.4%; Score 424; DB 1; Length 537;
Best Local Similarity 32.1%; Pred. No. 5e-23;
Matches 111; Conservative 59; Mismatches 138; Indels 38; Gaps 10;

Oy 3 KVDNN-TSQEGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATTY 61
Db 22 KLLMNLNDTEDIQVDEGFKLLLPVSYSVAVFWGLPLNIAAMWIFIAXMRPNWPTTVY 81

Oy 62 LVNLMVADLLYL-LPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSLILLTICISVHQ 120
Db 82 MFNLALSDTLVLSLPTLVVYADKNWPFGEVLCKLVFLFYANLYSSILFLTCISVHR 141

Oy 121 FLGVCHPLCSLYRTRHAWLGSTTVALVVLQPLTLAGSHDTYINGQMIWYDMSQEN 180
Db 142 YRGVCHRTSLRRNNAKHAHYICVIALVSVTLCLVFNLIFFVSPKVNVTCHITTRPED 201

Oy 181 FDLRFAY--GIVLTLSGF--LSLLGHFGVLFTDQGEPPDQARGEPHEDRQHSQVHPDHP 236
Db 202 FARVVEYSTAIMCLLFGIPCLIIAGCYGLMRELKMPVVS-----GNQQTLPYSYKRSIK 256

Oy 237 TGVWPLHPLFCALPYHSLLLPHLLSAFSGLPALDGSQC-----GLQDMEASGE 285
Db 257 T-----IIFVMAFAICFMFPHITRTLYYYARLLGKCVKALNVINVTYKVTREPLASANS 310

Oy 286 CEQLPQSPVLVSF-KGGKNNRVLRLQKRLQNGKLGHPAGRKRCPCGLN 330
Db 311 C-----IDPILYFLANDRYRRRLRTVRRRS-----SVPNRRCMHTN 347

RESULT 6
O7ZWQ7 XENLA PRELIMINARY; PRT; 537 AA.
AC O7ZWQ7 XENLA PRELIMINARY;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P2Y4-prov prov.
GN Name=p2ry4-prov.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.

TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initative.";
Dev. Dyn. 225:384-391(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
TISSUE=Embryo;
Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; BC046837; AAH46837.1; -; mRNA.
DR GO; GO:0016021; C:integral nucleotide receptor activity, G-...; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-...; IEA.
DR GO; GO:0004872; F:receptor-like activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000286; P2_purinocptor.
DR InterPro; IPR000018; P2Y4_purinocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01066; P2Y4RNOCPTR.
DR PRINTS; PR01157; P2Y4RNOCPTR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 537 AA; 61982 MW; B030F67D76CB9622 CRC64;

Query Match 23.3%; Score 422; DB 2; Length 537;
Best Local Similarity 32.1%; Pred. No. 7e-23;
Matches 110; Conservative 58; Mismatches 137; Indels 38; Gaps 10;

Oy 6 MN-TSQEGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATTYLVN 64
Db 25 MNLNTDTEICVDFEGFKLLLPVSYSVAVFWGLPLNIAAMWIFIAXMRPNWPTTVWFN 84

Oy 65 LMVADLLYL-LPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSLILLTICISVHFLG 123
Db 85 LALSDTLVLSLPTLVVYADKNWPFGEVLCKLVFLFYANLYSSILFLTCISVHYRG 144

Oy 124 VCHPLCSLYRTRHAWLGSTTVALVVLQPLTLAGSHDTYINGQMIWYDMSQENFDR 183
Db 145 VCHPITSLRRNNAKHAHYICVIALVSVTLCLVFNLIFFVSPKVNVTCHITTRPEDFAR 204
[1]
RP LFAY--GIVLTLSGF--LSLLGHFGVLFTDQGEPPDQARGEPHEDRQHSQVHPDHP 239
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Db 205 VVEYSTAIMCLLFGIPCLLIAGCYGLMTRMLKPIVS-----GNQOTLPSYKRSIKT-- 257
 Qy 240 WPLHPLFCALPHSLLLPHLLLSAFSGLPALDGSOC-----GLQMEASGECEQ 288
 Db 258 ----IIFMIAFAICFMPFHTRITLYYYARLIGIKYALNVINVTYKTRPLASANS-- 311
 Qy 289 LPQSPSPVLSF-KGGKNRVRLQKLRQKLGHPAGKRCPCGLN 330
 Db 312 ---IDPILYFLANDRYRRRLIRTVRRS-----SVNRRRCMTN 347

RESULT 7

ID Q4SELS_TETNG PRELIMINARY; PRT; 310 AA.
 AC Q4SELS;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 10 SCAP14616, whole genome shotgun sequence.
 DE (Fragment)
 GN ORFNames=GSTENG00019499001;

OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;

[1]

RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer S., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lucifalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Bienmont C., Skalli Z., Cattellico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).

[2]

RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB01014616; GACG00917.1; -; Genomic_DNA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR002286; P2_purnoceptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01157; P2YPURNOCPTR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT NON_TER 1
 FT NON_TER 310 310
 SQ SEQUENCE 310 AA; 35979 MW; DC6DF8ADB949D176 CRC64;

Query Match 23.2%; Score 420.5; DB 2; Length 310;
 Best Local Similarity 34.1%; Pred. No. 5, 2e-23;
 Matches 109; Conservative 52; Mismatches 122; Indels 37; Gaps 10;

Qy 15 CQFSEKYQVYLSLAYSIIIFILGLPLNGTVLHFHWGQTKRSCATYLVNVLADLVYL 74
 Db 3 CKFKEDFKYILLPVSYALVFVFLGLALNGLALVIVFRTKAWKPSVTFMFLTMCDTLYL 62

Qy 75 -LPFLIITYSDDRPFGECLKVHFLFYINLYGSIILLTCTISVHOFGLVCHPLCSLPY 133
 Db 63 TLPFLIITYYADENWPSEPFCKIIRLFYANLYGSIILFLCCISLHRIGVCYPRSLYW 122
 Qy 134 RTRHRLMGTSTTVALVQLLPTLAFSHTDYINGQIMWIYDMTQENFDRLFYAYGLVTL 193
 Db 123 LSARRAKFISVAVWAVLSCQSPVLVSFIRKDKNSRICYDTTSPFLFDDFLVYSSVISV 182
 Qy 194 SGFLSLILGHFGVLFDTG-----QEPQARG--EPHEDRQHSPOVHPDHTGWP 241
 Db 183 LMF--ALPFMTVMVCMGMLVWKLLLEVSRGAKRGNLSAROSKRSVKMIIVLATF--- 237
 Qy 242 LHPLFCALPHSLLLPHLLLSAFSGLPALDGSQ--CGLQDMEASGECEQLPOP----- 292
 Db 238 ---MLCFLPFH--LTRSLYSPFYIRQVNPHQITCGM--LEAINVAKVTRPLASANS 289
 Qy 293 -SPVLSFKGKN-RVRLQK 310
 Db 290 LDPILYFLAGQDIRSNLTKK 309

RESULT 8

OSBJ79_XENTR PRELIMINARY; PRT; 543 AA.
 AC OSBJ79;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Hypothetical protein.
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus; Silurana.
 OX NCBI_TaxID=8364;

[1]

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hirschman S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

NUCLEOTIDE SEQUENCE.

RP TISSUE=Embryo;

RA Klein S., Gerhard D.S.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; BC091589; AAH91589.1; -; mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-..; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR002286; P2_purnoceptor.

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DR InterPro: IPR000018; P2Y4_purinocptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOODPSN.
DR PRINTS: PR01066; P2Y4PRNOCPTR.
DR PRINTS: PR01157; P2Y4PRNOCPTR.
DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
SQ SEQUENCE 543 AA; 62234 MW; 23BD2FD005C3B901 CRC64;

Query Match 22.7%; Score 411; DB 2; Length 543;
Best Local Similarity 30.8%; Pred. No. 4.6e-22;
Matches 108; Conservative 63; Mismatches 126; Indels 54; Gaps 12;

Qy 8 TSQSGQLCQFSEKYQVLSIAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMV 67
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
24 TNNTEDESCVFNEGFKFLLPISYSGVFMVGLPLNITAIWIFIAKRPWNPPTVYMFNLAL 83
Qy 68 ADLLIYVL-LPFLIITYSLDRWPFGELLCKLVHFLFYINLYGSLILITCISVHQFLGVCH 126
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
84 SDTLVLSLPTLVYVYADQNNWPFQVLCIKVRELFYANLYSSILFTLCISVHRYGVCH 143
Qy 127 PLCSLPYRTRRHAMLGSTTVALVQLLPTLAF-SHTDXYINGQMIWYDMTSQENEDRLF 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
144 PITTLCRNAGAHVICALVWLSVNLCLVFMFMFTVSPKVG-TICHTDTLPEFDKYV 202
Qy 186 AY--GIVLTLSGF--LSILGHFGLFTDGOEPDQARGEPEHEDRQHSQVHPDPTGWGP 241
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
203 EYSTGIMCLLFGIFCLIIACCYGLMARELMKP-----LVNGNHQT--LP 244
Qy 242 LHP-----LFCALPYHSLLLPHLLSAFGLPALDGSQCG-----LQDWEAS 283
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
245 SYKRSIKTIIVIVMIAFAICMPFHITRTLYYARLLGVNVCYALNVINFTYKTRPLASA 304
Qy 284 GECEQLPPSPVLSF-KGKNRVRLLOKRLONKLGEPHAGKRGCPGLNRSG 333
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
305 NSC-----IDPILYFLANDRYRRRLIRTVRKSSV-----HHRCMWNHHPG 345

RESULT 9
Q4SEL9_TETNG PRELIMINARY; PRT; 308 AA.
AC Q4SEL9_TETNG
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 10 SCAF14616, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00019495001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallou O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Desilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castellillo V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).

```

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[2]
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014616; CAG00913.1; -; Genomic_DNA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR InterPro; IPR002286; P2_purinocptor.
DR InterPro; IPR000371; P2Y3_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOODPSN.
DR PRINTS; PR01066; P2Y3PRNOCPTR.
DR PRINTS; PR01157; P2Y4PRNOCPTR.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 308
SQ SEQUENCE 308 AA; 35563 MW; F71391660FCF8053 CRC64;

Query Match 22.4%; Score 405.5; DB 2; Length 308;
Best Local Similarity 33.3%; Pred. No. 6.6e-22;
Matches 92; Conservative 40; Mismatches 103; Indels 41; Gaps 6;

Qy 15 CQSEKYQVLSIAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLYVL 74
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
3 CTYKDFKRILLPAVTVTLVLLGLPLNAVILKTRPNLNRNNIYMLNLAIADFLYVT 62
Qy 75 -LPFLIITYSLDRWPFGELLCKLVHFLFYINLYGSLILITCISVHQFLGVCHPLCSLPY 133
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
63 SLPLIINYSGRDYWPFGELTCKLVRFQFYSNLSLFTLCISVQRYGVGICHPLANWHK 122
Qy 134 R-TRRHAWLGTSTTVALVQLLPTLAFSHTDXYINGQMIWYDMTSQENEDRLFAYGILT 192
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
123 RGRKMAWRVCGAVLLIVIALCAPTFHFAETGIGRNRVTCYDLSTPARSVDYYPYGMALT 182
Qy 193 LSGF-LSLLG-----HFQVLTGDEPQARGEPEHEDRQHSQVHPD 234
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
183 CLGFVLPFLGLVMVGYCRMAQILCRPVSYRGVSMATGEKDKA----- 224

235 HPTGVWPHPLFCA--LPYHSLLLPHLLSAFSGLP 268
225 -VNMIIVAAVFCISFLPFHFTKTVVMVRSIQMP 259

RESULT 10
P2RY6_RAT
ID P2RY6_RAT STANDARD; PRT; 328 AA.
AC Q6337L;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinocptor 6 (P2Y6).
GN Name=P2ry6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Arctic smooth muscle;
RX MEDLINE=96064682; PubMed=7592819; DOI=10.1074/jbc.270.44.26152;
RA Chang K., Hanaoka K., Kumada M., Takawa Y.;
RA "Molecular cloning and functional analysis of a novel P2 nucleotide
RT receptor."
RL J. Biol. Chem. 270:26152-26158(1995).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Heart;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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Db      180 LSPPLSTRYLIPYGNALTYIGFLPFTALLACVCRMARRLCRDGGPAGPVQARRSKAAR 231
QY      231 VHPDPTGWLPLHPLFCALPVHSLHLLPHLL-SAFSGLPALDQSGCGLQDMEASGCEQL 289
Db      240 M-----AVVAAFEVISFLPHITKTAYLAVRSTPGVSCPVLETFAAYKGT 287
QY      290 PQPS-----PVLSP----KGGKNRVLLOKL 311
Db      288 PFASANSVLDPILFVFTQOKFRQPHDLOKL 319

RESULT 11
P2RY6 MOUSE
ID      P2RY6 MOUSE      STANDARD;      PRT;      328 AA.
AC      Q9ERK9;
DT      05-JUL-2004 (Rel. 44, Created)
DT      05-JUL-2004 (Rel. 44, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      P2Y purinoceptor 6 (P2Y6).
DE      Name=P2ry6;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
NC      (1)
RN      NUCLEOTIDE SEQUENCE.
RP      STRAIN=129/SvEv;
RC      MEDLINE=21160052; PubMed=11259526;
RX      Lazarowski E.R., Rochelle L.G., O'Neal W.K., Ribeiro C.M.P.,
RA      Grubb B.R., Zhang V., Harden T.K., Boucher R.C.;
RA      "Cloning and functional characterization of two murine uridine
RT      nucleotide receptors reveal a potential target for correcting ion
RT      transport deficiency in cystic fibrosis gallbladder.";
RT      J. Pharmacol. Exp. Ther. 297:43-49(2001).
RN      (2)
RN      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP      STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krywinski M.I., Skalek U., Smallos D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -!- FUNCTION: Receptor for extracellular UTP > ADP = 2-methylthio-ATP
CC      > ADP-beta-S > ATP = ATP-gamma-S. The activity of this receptor is
CC      mediated by G proteins which activate a phosphatidylinositol-
CC      calcium second messenger system. Functionally coupled to
CC      phospholipase C (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is no
CC      removed.

```


[4]
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Kidney, and Leukocyte;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RX Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
 activate a phosphatidylinositol-calcium second messenger system.
 CC The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
 CC = ADP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Spleen, testis, kidney, liver, lung, heart and
 CC brain.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; U07225; AAC04923.1; -; mRNA.
 CC EMBL; AY136753; AA01279.1; -; mRNA.
 CC EMBL; BC012104; AA012104.1; -; mRNA.
 CC EMBL; BC028135; AA028135.1; -; mRNA.
 CC HSSP; P34996; 1DDO.
 CC Ensembl; ENSG00000175591; Homo sapiens.
 CC HGNC; HGNC:8541; P2RY2.
 CC H-InvDB; HIX0009916; -.
 CC MIM; 600041; -.
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0004872; F: receptor activity; TAS.
 CC GO; GO:0006873; P: cell ion homeostasis; TAS.
 CC GO; GO:0007200; P: G-protein signaling, coupled to IP3 second . . . ; TAS.
 CC InterPro; IPR002276; GPCR_Rhodopsn.
 CC InterPro; IPR002286; P2_purinocptor.
 CC InterPro; IPR003356; P2U_purinocptor.
 CC Pfam; PF00001; 7tm_1; 1.
 CC PRINTS; PR00237; GPCR_Rhodopsn.
 CC PRINTS; PR00594; P2Y2_P2Y2_P2Y2.
 CC PRINTS; PR01157; P2Y2_P2Y2_P2Y2.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 CC Transmembrane.
 KW TOPO_DOM 1 32 Extracellular (Potential).
 KW TRANSMEM 33 59 1 (Potential).
 FT TOPO_DOM 60 70 Cytoplasmic (Potential).
 FT TRANSMEM 71 93 2 (Potential).
 FT TOPO_DOM 94 110 Extracellular (Potential).
 FT TRANSMEM 111 129 Extracellular (Potential).
 FT TOPO_DOM 130 152 Cytoplasmic (Potential).
 FT TRANSMEM 153 172 4 (Potential).
 FT TOPO_DOM 173 194 Extracellular (Potential).
 FT TRANSMEM 195 220 5 (Potential).

FT TOPO_DOM 221 246 Cytoplasmic (Potential).
 FT TRANSMEM 247 269 6 (Potential).
 FT TOPO_DOM 270 287 Extracellular (Potential).
 FT TRANSMEM 288 309 7 (Potential).
 FT TOPO_DOM 310 377 Cytoplasmic (Potential).
 FT CARBOHYD 9 9 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
 FT DISULFID 106 183 By similarity.
 FT CONFLICT 312 312 R -> S (in Ref. 4; AA012104).
 FT CONFLICT 350 350 E -> G (in Ref. 1).
 FT CONFLICT 359 359 S -> F (in Ref. 1).
 SQ SEQUENCE 377 AA; 42290 MW; EE557A857A269AC6 CRC64;
 Query Match. 21.8%; Score 395.5; DB 1; Length 377;
 Best Local Similarity 33.0%; Pred. No. 4.4e-21;
 Matches 118; Conservative 41; Mismatches 118; Indels 81; Gaps 13;
 QY 15 CQSEKYQVYLSAYSIIFILGLPLNGTVLWHPGQTKWSCATTVLVNLMVADLLVYL 74
 Db 25 CRNEDFKYLLPVSGVGVVGLCLNVALYIFLCRLKTNASTTTFHFLAVSDALYAA 84
 QY 75 -LPFLIITYSLDRWPFGELLCKLVHFLFYINLYGSILLTCTISVHQLGVCPLCLSLPY 133
 Db 85 SLPLLVYVYARGDHPWPFSTVLCVRLFYTNLYCSILFJTCISVHRCGLVRLSLRW 144
 QY 134 RTRHAWLGSTTVALVQLLPTLAFSTHDYINGMIWYDMSQENFDLFAIGIVLTL 193
 Db 145 GRARYARRVAGAVVWLACQAPVLYFVTTSARGRVTCHTDTSAPELFSFVAYSSVM-- 202
 QY 194 SGFLSLHGFGVLF-----TDGQEPDQARGEPHEDRQHSQVHP 233
 Db 203 ---LGLL--FAVPFAVILVCVLMARLLKPAVGTSG-----GLPRAKKSVRT-- 246
 QY 234 DHPGTGVWPLPLF--CALPYH-----SLLLPHLLSAFS-----GLPALDGSQCG 276
 Db 247 -----IAVLAVPALCFELPEHVTTLTYSPSLDLSCHTLNAINMAYKVRPLASANS- 300
 QY 277 LQDMEASGECEQLPQSPSVLSFGKGNRVLLQKLRQNLKGEHPA--GRKRCPLGNS 332
 Db 301 -----LDPVLYFLAGQLRVFARDAKP-PTGSPATPARRRL-GLRRS 341
 RESULT 15
 ID P2RY4_MOUSE STANDARD; PRT; 361 AA.
 AC Q9JJS7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE P2Y purinocceptor 4 (P2Y4).
 GN Name=P2RY4; Synonyms=P2Y4r;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/SWJ;
 RX MEDLINE=21185993; PubMed=11290369; DOI=10.1016/S0014-2999(01)00875-5;
 RA Suarez-Huerta N., Pouillon V., Boeynaems J.-M., Robaye B.;
 RT "Molecular cloning and characterization of the mouse P2Y4 nucleotide
 RT receptor.";
 RL Eur. J. Pharmacol. 416:197-202 (2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; Tissue=Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragapi T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmer T., Guscinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Nunata K., Okido T., Pavan W.J., Perte G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi J., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shimada M.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shira T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002)."
CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC activate a phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the liver, intestine, stomach,
CC bladder and lung.
CC -!- PTM: Phosphorylation of Ser-329 and Ser-330 is a key step in
CC agonist-dependent desensitization and loss of surface P2RY4. This
CC phosphorylation does not involve PKC, nor other calcium-activated
CC kinases (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC EMBL: AJ277752; CAB91043.1; -; Genomic_DNA.
CC EMBL: AK076364; BAC36314.1; -; mRNA.
CC HSPB; P34996; iDDD.
CC
CC Ensembl: ENSMUSG00000044359; Mus musculus.
CC MGI: MGI:1926594; P2ry4.
CC GO: GO:0016021; C:integral to membrane; TAS.
CC GO: GO:0019103; F:pyrimidine nucleotide binding; IC.
CC GO: GO:0045030; F:UTP-activated nucleotide receptor activity; IDA.
CC GO: GO:0030321; F:trans epithelial chloride transport; IDA.
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC InterPro: IPR002286; P2_purinocptor.
CC InterPro: IPR000018; P2Y4_purinocptor.
CC Pfam: PF00001; 7tm_1; 1.
CC PRINTS: PR00237; GPCRHOOPS.
CC PRINTS: PR01066; P2Y4PNOCPTR.
CC PRINTS: PR01157; P2Y4PNOCPTR.
CC PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE: PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC
CC G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
CC Transducer; Transmembrane.
CC
CC TOPO_DOM 1 30 Extracellular (Potential).
CC TRANSMEM 31 58 1 (Potential).
CC TOPO_DOM 59 68 Cytoplasmic (Potential).
CC TRANSMEM 69 91 2 (Potential).
CC TOPO_DOM 92 108 Extracellular (Potential).
CC TRANSMEM 109 127 3 (Potential).
CC TOPO_DOM 128 149 Cytoplasmic (Potential).
CC TRANSMEM 150 170 4 (Potential).
CC TOPO_DOM 171 192 Extracellular (Potential).
CC TRANSMEM 193 218 5 (Potential).
CC TOPO_DOM 219 242 Cytoplasmic (Potential).
CC TRANSMEM 243 265 6 (Potential).

FT	TOPO_DOM	266	283	Extracellular (Potential).
FT	TRANSMEM	284	305	7 (Potential).
FT	TOPO_DOM	306	361	Cytoplasmic (Potential).
FT	MOD_RES	329	329	Phosphoserine (By similarity).
FT	MOD_RES	330	330	Phosphoserine (By similarity).
FT	CARBOHYD	175	175	N-linked (GlcNAc. .) (Potential).
FT	DISULFID	104	181	By similarity.
SQ	SEQUENCE	361 AA;	41034 MW;	358EA84B65BC0A20 CRC64;

Query Match 21.7%; Score 394; DB 1; Length 361;
Best Local Similarity 31.9%; Pred. No. 5.5e-21;
Matches 108; Conservative 55; Mismatches 134; Indels 42; Gaps 10;

Qy	9	SOEGLCOFSKDYKOVVLSLAYSIIIFILGLPLNGVLMWHFWGQTKRWSCATTYLVNLMVA	68
Db	17	SSGDGCKNFEEFKFILLPLSLVAVVVLGLALNAPTLLWFLFLRUPWDATATYMFHLALS	76
Qy	69	DLLYVL-LPFLIIITYSLDDRPFGELCKLVHFLFYINLYGSIIILLTICISVHQFLGVCHP	127
Db	77	DTLYVLSLPTLVVYVYAAARNHWPFGTGCKFVRFVFNWLYCSVLELTICISVHRYMGICHP	136
Qy	128	LCSLPYTRRRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQENFDR--LP	185
Db	137	LRAIRWGRPRPAGLLCLGVMLVAGCLVPLNLFVTTNANGTTILCHDTTLPEEFHYVVF	196
Qy	186	AYGIVLTLSG--FLSLCHFGVLTGQEPDQARGEHEDHQSPSOVHPDPTGVWPLH	243
Db	197	SSTIMVLLFGFPFLITLVYGLMARRLYRPLPGAGQ-----SSRLR-----SLR	241
Qy	244	PLFCALPVHSL-LLPHLLLSAFSGLPALDGSQGL-----QDMEASGECEQLPQ	291
Db	242	TIADVLTFAVCFVFFHITRIYVILARLLNAECRVLNIWVYKVTPLASNSC-----	296
Qy	292	PSPVL-SFKGKNNRVLQKLQKLNKLGHPHAGRKRCPLG	329
Db	297	LDPVLYLFTGDKYRNQLQCLCR---GSTPKRRITASSL	331

Search completed: February 13, 2006, 14:42:17
Job time : 234 secs

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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:35:04 ; Search time 186 Seconds
(without alignments)
786.630 Million cell updates/sec

Title: US-10-088-726-20
Perfect score: 1812
Sequence: 1 MEKVDMTSQQGLQCFSEK.....NKLGEHPAGKRCPLGNRSG 333

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1812	100.0	333	4	AAG64125 Human G p
2	1804	99.6	361	7	AB99264 Human P2Y
3	1798	99.2	360	5	AB998145 Human GPC
4	1536	84.8	295	5	AAU11251 Human P2Y
5	1397	77.1	361	5	AD116630 Human NOV
6	1387	76.5	361	8	ADN42284 Human nov
7	1051	58.0	338	7	ADC26009 Human pur
8	1051	58.0	338	7	ABW00804 Human GPC
9	1047	57.8	339	5	AB998146 Human GPC
10	1047	57.8	339	5	AAE18640 Human G-p
11	1047	57.8	339	8	ADQ30394 Human GPC
12	1041	57.5	338	7	ADC26000 Human pur
13	936	51.7	271	7	ADC86167 Human GPC
14	921	50.8	170	4	AA880935 Human nGP
15	921	50.8	170	5	ABG93753 Human G p
16	779	43.0	302	8	ADQ30396 Mouse GPC
17	749	42.8	328	5	AD116984 NOVX prot
18	749	42.8	328	5	AD116983 NOVX prot
19	449	24.8	328	8	ADP49191 Chick P2Y
20	449	24.8	328	8	ADR89634 Chick P2Y
21	429	23.7	374	4	AAE04390 Turkey NO
22	429	23.7	374	5	AD116982 Turkey P2
23	429	23.7	374	8	ADR89631 Turkey G-
24	424	23.4	537	5	AAU74538 Human P2Y

25	424	23.4	537	5	AD116981	Adi16981 Human NOV
26	424	23.4	537	8	ADR89632	Adr89632 Xenopus P
27	402.5	22.2	377	4	AAE01144	Aae01144 Human pur
28	402	22.2	328	7	ADD45304	Add45304 Rat Prote
29	397	21.9	328	2	AAR91224	Aar91224 Mouse pan
30	397	21.9	328	7	ADC37339	Adc37339 Nuclear f
31	397	21.9	328	8	ADO29601	Ado29601 Mouse GPC
32	396	21.9	361	5	AD116985	Adi16985 Rat NOVX
33	396	21.9	361	7	ADH69290	Adh69290 Rat orpha
34	396	21.9	361	8	ADF91782	Adf91782 Rat orpha
35	396	21.9	361	8	ADR89629	Adr89629 Rat G-pro
36	396	21.9	361	8	ADS84264	Ads84264 Rat G pro
37	395.5	21.8	377	4	AAE01143	Aae01143 Human P2-
38	395.5	21.8	377	6	AAE04392	Aae04392 Human pur
39	395.5	21.8	377	6	ABP81866	Abp81866 Human pur
40	395.5	21.8	377	7	ADE62766	Ade62766 Human Pro
41	395.5	21.8	377	8	ADO29596	Ado29596 Human GPC
42	395.5	21.8	377	8	ADP49189	Adp49189 Human pla
43	394.5	21.8	328	2	AAR91225	Aar91225 Human pla
44	394	21.7	361	8	ADO29599	Ado29599 Mouse GPC
45	389.5	21.5	328	4	AAE04393	Aae04393 Human P2-

ALIGNMENTS

RESULT 1
AAG64125
ID AAG64125 standard; protein; 333 AA.
XX
AC AAG64125;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human G protein-coupled receptor GPRV71.
XX

Human; guanosine triphosphate binding protein-coupled receptor;
KW GPRV71; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytostatic; hepatotropic; nootropic;
KW neuroprotective; gene therapy; peptide therapy.

OS Homo sapiens.

PN WO200148188-A1.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-JP009408.

PR 28-DEC-1999; 95JP-00375152.

PR 31-MAR-2000; 2000JP-00101339.

XX (HELI-) HELIX RES INST.

PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;

PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;

DR WPI; 2001-425662/45.

XX N-PSDB; AAH73516.

XX New DNA encoding guanosine triphosphate binding protein coupled receptors
PT and their expression products for screening potential anticancer and
PT nootropic drugs and in diagnosis of these diseases.

PS Example 1; Page 132-135; 170pp; Japanese.

XX The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,

CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
 CC present sequence is a G protein-coupled receptor of the invention
 SQ Sequence 333 AA;

Query Match 100.0%; Score 1812; DB 4; Length 333;
 Best Local Similarity 100.0%; Pred. No. 7.4e-191;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVDNMTSBOGLCOFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60
 DB 1 MEKVDNMTSBOGLCOFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60

QY 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLTTCISVHQ 120
 DB 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLTTCISVHQ 120

QY 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGOMIWDMTSQEN 180
 DB 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGOMIWDMTSQEN 180

QY 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTGQEPDQARGEPEHEDRQHSQVHPDHPGTVW 240
 DB 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTGQEPDQARGEPEHEDRQHSQVHPDHPGTVW 240

QY 241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLDMEASGECEQLPQSPVLSFKG 300
 DB 241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLDMEASGECEQLPQSPVLSFKG 300

QY 301 GKNRVLLQKLQKLNKLGHEHPAGRCRCPLNRSG 333
 DB 301 GKNRVLLQKLQKLNKLGHEHPAGRCRCPLNRSG 333

RESULT 2
 ADB99264
 ID ADB99264 standard; protein; 361 AA.
 XX
 AC ADB99264;
 DT 04-DEC-2003 (first entry)
 DE Human p2Y2li protein.
 XX
 KW gene; human; P2Y2li; chromosome 3; G protein-coupled receptor; GPCR;
 KW Class A rhodopsin-like sub-family; gene therapy; receptor.
 XX
 OS Homo sapiens.
 XX
 PN DE10144044-A1.
 XX
 PD 27-MAR-2003.
 XX
 PF 07-SEP-2001; 2001DE-01044044.
 XX
 PR 07-SEP-2001; 2001DE-01044044.
 XX
 PA (BRUE/) BRUESS M.
 PA (BOEN/) BOENISCH H.
 PA (VKUE/) VON KUEGELGEN I.
 XX
 PI Bruess M, Boenisch H, Von Kuegelgen I;
 XX
 DR WPI; 2003-364675/35.
 DR N-PSDB; ADB99267.
 XX
 PT New human gene P2Y2li and encoded G protein-coupled receptor, useful for
 PT treatment and diagnosis of receptor-associated diseases and for drug
 XX screening.
 PS
 PS Disclosure; Page 4; 6pp; German.
 XX
 CC This invention describes the human P2Y2li gene and its 5'- and 3'-

CC untranslated regions, located on chromosome 3 which is a novel G protein-
 CC coupled receptor (GPCR). The protein encoded by P2Y2li is expressed in
 CC blood cells, testis and embryonal kidney cells and contains potential
 CC sites for phosphorylation by protein kinase C and casein kinase II. It is
 CC a member of the Class A rhodopsin-like sub-family of G protein-coupled
 CC receptors and it probably a nucleoside/nucleotide receptor that mediates
 CC action of nucleosides/nucleotides or their sugar derivatives. P2Y2li and
 CC antibodies directed against the encoded protein are useful in diagnosis
 CC and treatment (including gene therapy) of diseases associated with
 CC abnormal levels of P2Y2li expression, in screening assays for modulators,
 CC potential therapeutic agents, and to produce transgenic animals, e.g. for
 CC identifying diseases associated with abnormal expression of P2Y2li. This
 CC sequence represents the human P2Y2li protein described in the disclosure
 XX of the invention.
 SQ Sequence 361 AA;

Query Match 99.6%; Score 1804; DB 7; Length 361;
 Best Local Similarity 99.7%; Pred. No. 6.3e-190;
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEKVDNMTSBOGLCOFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60
 DB 29 MEKVDNMTSBOGLCOFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88

QY 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLTTCISVHQ 120
 DB 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLTTCISVHQ 148

QY 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGOMIWDMTSQEN 180
 DB 149 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGOMIWDMTSQEN 208

QY 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTGQEPDQARGEPEHEDRQHSQVHPDHPGTVW 240
 DB 209 FDLRFAYGIVLTLSGFLSLGLHFGVLTGQEPDQARGEPEHEDRQHSQVHPDHPGTVW 268

QY 241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLDMEASGECEQLPQSPVLSFKG 300
 DB 269 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLDMEASGECEQLPQSPVLSFKG 328

QY 301 GKNRVLLQKLQKLNKLGHEHPAGRCRCPLNRSG 333
 DB 329 GKNRVLLQKLQKLNKLGHEHPAGRCRCPLNRSG 361

RESULT 3
 ABB98145
 ID ABB98145 standard; protein; 360 AA.
 XX
 AC ABB98145;
 DT 17-OCT-2002 (first entry)
 DE Human GPCR designated PFI-020.
 XX
 KW Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
 KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
 KW disorder; PFI-020.
 XX
 OS Homo sapiens.
 XX
 PN EP1215214-A1.
 XX
 PD 19-JUN-2002.
 XX
 PF 04-DEC-2001; 2001EP-00310137.
 XX
 PR 18-DEC-2000; 2000GB-00030855.
 PR 17-JAN-2001; 2001GB-00001222.
 XX
 PA (PFIZ) PFIZER LTD.
 PA (PFIZ) PFIZER INC.

XX Fidock MD;
 XX WPI; 2002-510798/55.
 DR N-PSDB; ABQ76000.
 XX
 PT New polynucleotide encoding G protein-coupled receptor PFI-020, useful
 PT e.g. for treating eating and sleeping disorders and for identifying
 PT specific modulators.
 XX
 XX Claim 1 (a); Page 11-12; 23pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a novel
 CC polypeptide belonging to the class of proteins known as G-protein coupled
 CC receptors (GPCRs). The activity of proteins of the invention may be
 CC described as, antidepressant and neuroleptic. Polynucleotides of the
 CC invention are used for recombinant expression of the G protein-coupled
 CC receptor (PFI-020) polypeptides, to create transgenic animals, as source
 CC of primers, probes, antisense sequences and ribozymes and in gene
 CC therapy. Therapeutic agents of the invention can be used to treat a wide
 CC range of disorders, particularly mood disorders, depression or arousal,
 CC especially eating and sleeping disorders. The current sequence represents
 CC a human GPCR designated PFI-020
 XX
 XX Sequence 360 AA;
 PS
 Query Match 99.2%; Score 1798; DB 5; Length 360;
 Best Local Similarity 99.7%; Pred. No. 2.9e-189;
 Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MEKVDNMTSQBGLCFQSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
 DB 29 MEKVDNMTSQBGLCFQSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
 QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLKLVHFLFYINLYGSILLTLCISVHQ 120
 DB 89 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLKLVHFLFYINLYGSILLTLCISVHQ 148
 QY 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMIWYDMTSOEN 180
 DB 149 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMIWYDMTSOEN 208
 QY 181 FDRLPFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPEHEDROHSPSQVHPDPTGVW 240
 DB 209 FDRLPFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPEHEDROHSPSQVHPDPTGVW 268
 QY 241 PLHPLFCALPYHSLLLPHLLSAFSLGSLPALDGSQGLQDMEASGCEQLPQSPVLSFKG 300
 DB 269 PLHPLFCALPYHSLLLPHLLSAFSLGSLPALDGSQGLQDMEASGCEQLPQSPVLSFKG 328
 QY 301 GKNRVLLQKLQKRNKLGHPAGKRCPCGLNRS 332
 DB 329 GKNRVLLQKLQKRNKLGHPAGKRCPCGLNRS 360
 RESULT 4
 AAU11251
 ID AAU11251 standard; protein; 295 AA.
 XX
 AC AAU11251;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE Human P2Y-like G protein-coupled receptor.
 XX
 KW Human; P2Y-like G protein-coupled receptor; GPCR; COPD;
 KW chronic obstructive pulmonary disease; nervous system disease;
 KW Parkinson's disease; multiple sclerosis; dementia; stroke;
 KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;
 KW bacterial infection; fungal infection; protozoan infection;
 KW viral infection; pain; cancer; anorexia; bulimia; asthma;
 KW acute heart failure; hypertension; hypertension; osteoporosis; diabetes;
 KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;

KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KW manic depression; delirium; severe mental retardation; dyskinesia.
 XX
 OS Homo sapiens.
 XX
 PN WO200185764-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 09-MAY-2001; 2001WO-EP005244.
 XX
 PR 11-MAY-2000; 2000US-0203582P.
 PR 21-FEB-2001; 2001US-0269857P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI; 2002-075242/10.
 DR N-PSDB; AAS17746.
 XX
 PT New polynucleotides for producing P2Y-like G protein-coupled receptors
 PT (GPCR) that are used for screening inhibitors or regulators of human P2Y-
 PT like GPCR, especially useful for treating pain, cancer or neurological
 PT disorders.
 XX
 PS Claim 25; Fig 2; 114pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a P2Y-like G
 CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or
 CC allele, a host cell containing an expression vector comprising the
 CC polynucleotide and screening for agents that regulate the GPCR activity.
 CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide, human
 CC which may be employed for screening agents that inhibit or regulate human
 CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is
 CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly
 CC COPD (chronic obstructive pulmonary disease), peripheral or central
 CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,
 CC dementia, stroke, Alzheimer's disease and many other diseases and
 CC disorders listed in the specification), benign prostatic hyperplasia or
 CC urinary incontinence. A pharmaceutical composition containing the
 CC modulators and/or regulators of P2Y-like GPCR is useful for modulating
 CC the activity of a P2Y-like GPCR. In particular, these are useful for
 CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,
 CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,
 CC acute heart failure, hypertension, hyperextension, osteoporosis, diabetes,
 CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,
 CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic
 CC depression, delirium, severe mental retardation or dyskinesias). The
 CC present sequence is the P2Y-like GPCR of the invention

Sequence 295 AA;

Query Match 84.8%; Score 1536; DB 5; Length 295;
 Best Local Similarity 98.3%; Pred. No. 1.9e-160;
 Matches 283; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVDNMTSQBGLCFQSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
 DB 1 MEKVDNMTSQBGLCFQSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
 QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLKLVHFLFYINLYGSILLTLCISVHQ 120
 DB 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLKLVHFLFYINLYGSILLTLCISVHQ 120
 QY 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMIWYDMTSOEN 180
 DB 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMIWYDMTSOEN 180
 QY 181 FDRLPFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPEHEDROHSPSQVHPDPTGVW 240
 DB 181 FDRLPFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPEHEDROHSPSQVHPDPTGVW 240

Qy 241 PLHPLFCALPVHSLLLPHLLLSAFSLPALDGSQGLQDMASGECEQ 288
 Db 241 PLHPLFCALPVHSLLLPHLLLSAFSLPALDGSQGLQDMASVKAMQ 288

RESULT 5
 ID AD116630 standard; protein; 361 AA.
 XX AC AD116630;
 XX DT 15-APR-2004 (first entry)
 XX DE Human NOVX protein to treat human pathological conditions SeqID166.
 XX KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;
 KW inflammation; autoimmune disorder; allergy; blood disorder;
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;
 KW cytosolic; cardiac; antiinflammatory; immunosuppressive; antiallergic;
 KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;
 KW antiasthmatic; nephrotropic; antiarthritic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;
 KW chromosome mapping; tissue typing; pharmacogenomic; SNP;
 KW single nucleotide polymorphism.
 XX OS Homo sapiens.
 XX PN WO200268649-A2.
 XX PD 06-SEP-2002.
 XX PF 31-JAN-2002; 2002WO-US002785.
 XX PR 31-JAN-2001; 2001US-0285395P.
 PR 31-JAN-2001; 2001US-0285412P.
 PR 31-JAN-2001; 2001US-0265514P.
 PR 31-JAN-2001; 2001US-0265517P.
 PR 02-FEB-2001; 2001US-0266406P.
 PR 05-FEB-2001; 2001US-0266767P.
 PR 07-FEB-2001; 2001US-0266975P.
 PR 07-FEB-2001; 2001US-0267057P.
 PR 08-FEB-2001; 2001US-0267459P.
 PR 09-FEB-2001; 2001US-0267823P.
 PR 15-FEB-2001; 2001US-0268974P.
 PR 26-FEB-2001; 2001US-0271664P.
 PR 27-FEB-2001; 2001US-0271839P.
 PR 27-FEB-2001; 2001US-0271855P.
 PR 02-MAR-2001; 2001US-0273046P.
 PR 14-MAR-2001; 2001US-0275925P.
 PR 14-MAR-2001; 2001US-0275947P.
 PR 14-MAR-2001; 2001US-0275950P.
 PR 14-MAR-2001; 2001US-0275989P.
 PR 15-MAR-2001; 2001US-0276448P.
 PR 16-MAR-2001; 2001US-0276450P.
 PR 16-MAR-2001; 2001US-0276397P.
 PR 20-MAR-2001; 2001US-0276768P.
 PR 20-MAR-2001; 2001US-0276852P.
 PR 26-MAR-2001; 2001US-0278775P.
 PR 26-MAR-2001; 2001US-0278788P.
 PR 29-MAR-2001; 2001US-0279882P.
 PR 29-MAR-2001; 2001US-0280147P.
 PR 30-MAR-2001; 2001US-0280147P.
 PR 11-APR-2001; 2001US-0282992P.
 PR 11-APR-2001; 2001US-0283063P.
 PR 20-APR-2001; 2001US-0285133P.
 PR 23-APR-2001; 2001US-0285749P.
 PR 03-MAY-2001; 2001US-0288327P.
 PR 03-MAY-2001; 2001US-0288504P.
 PR 29-MAY-2001; 2001US-0294047P.

PR 30-MAY-2001; 2001US-0294473P.
 PR 08-JUN-2001; 2001US-0296964P.
 PR 18-JUN-2001; 2001US-0298959P.
 PR 19-JUN-2001; 2001US-0299324P.
 PR 13-AUG-2001; 2001US-0312020P.
 PR 16-AUG-2001; 2001US-0312889P.
 PR 16-AUG-2001; 2001US-0312908P.
 PR 21-AUG-2001; 2001US-0313390P.
 PR 28-AUG-2001; 2001US-0315470P.
 PR 31-AUG-2001; 2001US-0316447P.
 PR 07-SEP-2001; 2001US-0318115P.
 PR 07-SEP-2001; 2001US-0318118P.
 PR 12-SEP-2001; 2001US-0318740P.
 PR 19-SEP-2001; 2001US-0323379P.
 PR 18-OCT-2001; 2001US-0330245P.
 PR 18-OCT-2001; 2001US-0330308P.
 PR 14-NOV-2001; 2001US-0332701P.
 XX (CURA-) CURAGEN CORP.
 PA Tthernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;
 XX Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CB;
 PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
 PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX WPI; 2002-706998/76.
 DR N-PSDB; AD116629.
 XX
 XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; SEQ ID NO 166; 1498pp; English.

XX This invention relates to a novel nucleic acids, and encoded polypeptides
 CC thereof, which have properties related to the stimulation of biochemical
 CC or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for
 CC diagnostic and prognostic assays and furthermore in the treatment of
 CC diverse pathological conditions. The present invention describes novel
 CC human and murine NOVX proteins, as well as methods to modulate their
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in
 CC treating or preventing diseases such as inflammation, autoimmune
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy,
 CC and epilepsy. Accordingly, these molecules have many activities including
 CC cytosolic, cardiac, antiinflammatory, immunosuppressive, antiallergic,
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,
 CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,
 CC relaxant and anticonvulsant. In addition, they are useful in screening
 CC assays to identify small molecules that modulate or inhibit, for example,
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also
 CC used as in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. This polypeptide is a human NOVX protein of the
 CC invention.

XX Sequence 361 AA;

Query Match 77.1%; Score 1397; DB 5; Length 361;
 Best Local Similarity 80.9%; Pred. No. 5.5e-145;
 Matches 275; Conservative 11; Mismatches 40; Indels 14; Gaps 5;

Qy 1 MEKVDNMTSQEQGLQCFSEKFKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
 |||||
 Db 29 MEKVDNMTSQEQGLQCFSEKFKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 88
 |||||
 Qy 61 YLVNLMVADLLYVLLPFLIITYSLSDRRWPFGLCKLVHFLFYINLYGSIILLTICISVHQ 120


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|||||
89 YLVNLMWADLLVLLPFLIITYSLDDRWPFGLCKLVHFLFYINLYGSIILLTCTSVHQ 148
QY 121 FLGVCHPLCSLPYRTRHAWLGSTTWALVVLQLLPTLAFSTHDYINGOMIWDMTSOEN 180
Db 149 FLGVCHPLCSLPYRTRHAWLGSTTWALVVLQLLPTLAFSTHDYINGOMIWDMTSOEN 208
QY 181 FDLRFAYGIVLTLGSLFLSLGHFGVLTDTGQEPDQARG--EPHEDRQHSQSVHPDHPHG 238
Db 209 FDLRFAYGIVLTLGSLFLSLGHFGVLSL-----WVRSLIKPEENIMRTGNTARARSIRT 262
QY 239 VMLPFLPFL--CALPYHSLLLPHHLSAF---SGLPALDGSQCGLQDMASGECEQLPQPS 293
Db 263 ILLVCGLFTLCFVPFH-ITRSFYLTICFLSDCOLLMAAQCGLODMASGECEQLPQPS 321
QY 294 PVLSPKGGKNNRVLRLQKLRQNLGSHHPAGKRCPCGLNRSRG 333
Db 322 PVLSPKGGKNNRVLRLQKLRQNLGSHHPAGKRCPCGLNRSRG 361

RESULT 6
ADN42284
ID ADN42284 standard; protein; 361 AA.
XX
AC ADN42284;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human novel proteinNOV 43.
XX
KW Human; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; SNP;
KW single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT Misc-difference 162
FT ;/note= "May be Pro as the result of a single nucleotide
FT polymorphism"
XX
PN US2004033493-A1.
XX
PD 19-FEB-2004.
XX
PF 31-JAN-2002; 2002US-00072012.
XX
PR 31-JAN-2001; 2001US-0265395P.
PR 31-JAN-2001; 2001US-0265412P.
PR 31-JAN-2001; 2001US-0265514P.
PR 31-JAN-2001; 2001US-0265517P.
PR 02-FEB-2001; 2001US-0266406P.
PR 05-FEB-2001; 2001US-0266767P.
PR 07-FEB-2001; 2001US-0266975P.
PR 07-FEB-2001; 2001US-0267057P.
PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 02-MAR-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.

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PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 29-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313930P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
(TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX
Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
PI Furtak K, Grosse WM, Alsobrook JP, Lapley DM, Rieger DK, Burgess CE;
XX
WPI; 2004-180039/17.
DR N-PSDB; ADN42283.
XX
Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX
Claim 1; SEQ ID NO 166; 1309pp; English.
XX
The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
CC vector, an antibody that binds immunospecifically to NOVX, determining
CC the presence or amount of NOVX in a sample, determining the presence or
CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,

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CC modulating the activity of NOVX, treating or preventing a NOVX-associated
CC disorder, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX and treating a pathological state
CC in a mammal comprising administering a polypeptide which is at least 95%
CC identical to NOVX (or fragment). NOVX and NA may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
CC detecting the presence of NOVX in samples (e.g. by enzyme linked
CC immunosorbant assay (ELISA). The agents and methods may be used in this
CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
CC and/or atherosclerosis. The present sequence represents a NOVX protein.
XX
SQ Sequence 361 AA;

Query Match 76.5%; Score 1387; DB 8; Length 361;
Best Local Similarity 80.6%; Pred. No. 7e-144;
Matches 274; Conservative 11; Mismatches 41; Indels 14; Gaps 5;
Qy 1 MEKVDNMTSQBQGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db 29 MEKVDNMTSQBQGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 120
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 148
Qy 121 FLGVCHPLCSLPYTRRHAWLGTSTTVALVQLPLTAFSHTDYINGQMIWYDWTQSEN 180
Db 149 FLGVSHPLCSLPYTRRHAWLGTSTTVALVQLPLTAFSHTDYINGQMIWYDWTQSEN 208
Qy 181 FDRLFAYGIVLTSGFLSLGHLGHFVLETDGQEPDQARG--EPHEDRQHSPSQVHPDPTG 238
Db 209 FDRLFAYGIVLTSGFLSLGHLGHFVYSL-----WVRSLIKPEENLRTGNTARARSIRT 262
Qy 239 VWPLHPLF--CALPYHSLLLPHLLLSAF---SGLPALDGSQCGLQDMASGECQLPQPS 293
Db 263 ILLVCGFLTLCFVFPFH-ITRSFYLTICFLLSQDCQLLMAAQGLQDMASGECQLPQPS 321
Qy 294 PVLSFKGKNRVRLQKLRQNKLGHPAGRKRCPCPLNRSG 333
Db 322 PVLSFKGKNRVRLQKLRQNKLGHPAGRKRCPCPLNRSG 361

RESULT 7
ID ADC26009 standard; protein; 338 AA.
XX
AC ADC26009;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human purinergic receptor P2Y-related GPCRx6 alternative protein.
XX
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
KW anorectic; cardiant; hypotensive; osteopathic; antianigmal;
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW human; GPCRx6; purinergic receptor P2Y.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 270
FT /note= "Encoded by TTC"
XX

PN US2003088080-A1.
XX
PD 08-MAY-2003.
XX
PF 21-JUN-2001; 2001US-00885453.
XX
PR 20-JUN-2000; 2000US-0212908P.
XX
PR 05-DEC-2000; 2000EP-00870289.
XX
XX (COMM// COMMUNI D.
XX (LANN// LANN V.
XX (GOVA// GOVAERTS C.
XX (PARM// PARMENTIER M.
XX (DETH// DETHUX M.
XX
XX Communi D, Lannoy V, Govaerts C, Parmentier M, Dethaux M;
XX
XX WPI: 2003-657983/62.
XX N-PSDB; ADC25999.
XX
XX New human G-protein coupled receptor, useful for treating receptor-
XX mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
XX acute heart failure, osteoporosis, stroke, ulcer, allergy, or
XX neurological disorders.
XX
XX Example 3; Page 15; 24pp; English.
XX
XX The invention relates to a novel G-protein coupled receptor (GPCR). The
XX receptor, polynucleotide, agonist, reverse agonist and antagonist of the
XX invention may be useful for treating receptor-mediated disorders
XX including viral, fungal or bacterial infections, immune-related disorders
XX such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
XX hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
XX ulcer and allergy, as well as psychotic and neurological disorders such
XX as schizophrenia and dementia, degenerative diseases such as Parkinson's
XX disease and Alzheimer's disease and dyskinesias such as Huntington's
XX disease. The current sequence is that of the human purinergic receptor
XX P2Y-related GPCRx6 alternative protein of the invention.
XX
SQ Sequence 338 AA;
Query Match 58.0%; Score 1051; DB 7; Length 338;
Best Local Similarity 98.0%; Pred. No. 8.1e-107;
Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MEKVDNMTSQBQGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db 29 MEKVDNMTSQBQGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 120
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 148
Qy 121 FLGVCHPLCSLPYTRRHAWLGTSTTVALVQLPLTAFSHTDYINGQMIWYDWTQSEN 180
Db 149 FLGVCHPLCSLPYTRRHAWLGTSTTVALVQLPLTAFSHTDYINGQMIWYDWTQSEN 208
Qy 181 FDRLFAYGIVLTSGFLSLG 200
Db 209 FDRLFAYGIVLTSGFLSLG 228
RESULT 8
ID ABW00804 standard; protein; 338 AA.
XX
XX AC ABW00804;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human GPCRx6 protein.
XX
XX Human; G-protein coupled receptor; GPCR; infection; neoplastic process;
KW

KW inflammation; myocardial infarction; atherosclerosis; angina pectoris;
 KW hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;
 KW diabetes; cancer; virucide; analgesic; cardiant.

XX Homo sapiens.

OS US2003108986-A1.

PN XX 12-JUN-2003.

PD XX 20-FEB-2002; 2002US-00079384.

PF XX 21-JUN-2001; 2001US-00885453.

PR XX (EURO-) EUROSREEN SA.

PA Communi D, Lannoy V, Brezillon S, Detheux M, Parmentier M;

PI Govaerts C;

PN WPI; 2003-810852/76.

DR N-PSDB; AAD61648.

XX Novel G-protein coupled receptor useful for treating viral infections,
 PT bacterial infections, fungal infections, cancer, diabetes, hypertension,
 PT osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.

PS Claim 1; Fig 4; Opp; English.

XX The present invention relates to novel G-protein coupled receptors
 CC (GPCRs) and the nucleic acids encoding them. The invention is useful for
 CC treating viral, bacterial and fungal infections, inflammatory and
 CC neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,
 CC angina pectoris, myocardial infarction and atherosclerosis. The present
 CC sequence is human G-protein coupled receptor (GPCR) protein

XX Sequence 338 AA;

Query Match 58.0%; Score 1051; DB 7; Length 338;

Best Local Similarity 98.0%; Pred. No. 8.1e-107; Mismatches 4; Indels 0; Gaps 0;

Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVDMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60

Db 29 MEKVDMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88

QY 61 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTTCISVHQ 120

Db 89 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTTCISVHQ 148

QY 121 FLGVCHPLCSLPYRTRRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 180

Db 149 FLGVCHPLCSLPYRTRRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 208

QY 181 FDRLFAYGIVLTLSGFLSLL 200

Db 209 FDRLFAYGIVLTLSGFFPSL 228

RESULT 9

ABB98146

ID ABB98146 standard; protein; 339 AA.

XX ABB98146;

AC ABB98146;

XX 17-OCT-2002 (first entry)

XX Human GPCR designated PFI-020'.

XX Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
 KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
 KW disorder; PFI-020'.

XX Homo sapiens.

XX EP1215214-A1.

PN 19-JUN-2002.

PD 04-DEC-2001; 2001EP-00310137.

PF 18-DEC-2000; 2000GB-00030855.

PR 17-JAN-2001; 2001GB-00001222.

XX (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

XX Fidoock MD;

XX WPI; 2002-510798/55.

DR N-PSDB; ABQ79300.

XX New polynucleotide encoding G protein-coupled receptor PFI-020, useful
 PT e.g. for treating eating and sleeping disorders and for identifying
 PT specific modulators.

PS Claim 1 (b); Page 13; 23pp; English.

XX The invention relates to an isolated polynucleotide encoding a novel
 CC polypeptide belonging to the class of proteins known as G-protein coupled
 CC receptors (GPCRs). The activity of proteins of the invention may be
 CC described as, antidepressant and neuroleptic. Polynucleotides of the
 CC invention are used for recombinant expression of the G protein-coupled
 CC receptor (PFI-020) polypeptides, to create transgenic animals, as source
 CC of primers, probes, antisense sequences and ribozymes and in gene
 CC therapy. Therapeutic agents of the invention can be used to treat a wide
 CC range of disorders, particularly mood disorders, depression or arousal,
 CC especially eating and sleeping disorders. The current sequence represents
 CC a human GPCR designated PFI-020'

XX Sequence 339 AA;

Query Match 57.8%; Score 1047; DB 5; Length 339;

Best Local Similarity 99.0%; Pred. No. 2.3e-106;

Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEKVDMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60

Db 29 MEKVDMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88

QY 61 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTTCISVHQ 120

Db 89 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTTCISVHQ 148

QY 121 FLGVCHPLCSLPYRTRRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 180

Db 149 FLGVCHPLCSLPYRTRRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 208

QY 181 FDRLFAYGIVLTLSGFLS 198

Db 209 FDRLFAYGIVLTLSGFLS 226

RESULT 10

AAE18640

ID AAE18640 standard; protein; 339 AA.

XX AAE18640;

AC AAE18640;

XX 17-MAY-2002 (first entry)

XX Human G-protein coupled receptor (GCREC-1).

XX Human; G-protein coupled receptor; GCREC-1; cell proliferative disorder;
 KW neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;
 KW metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;
 KW Pick's disease; Huntington's disease; Parkinson's disease; hypertension;

CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia;
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 339 AA;

Query Match 57.8%; Score 1047; DB 8; Length 339;
 Best Local Similarity 99.0%; Pred. No. 2.3e-106;
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKYDMNTSQOGLCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
 Db 29 MEKYDMNTSQOGLCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
 Qy 61 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCTISVHQ 120
 Db 89 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCTISVHQ 148
 Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSEN 180
 Db 149 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSEN 208
 Qy 181 FDRLPFAYGIVLTLSGFLS 198
 Db 209 FDRLPFAYGIVLTLSGFLS 226

RESULT 12

ADC26000
 ID ADC26000 standard; protein; 338 AA.

AC ADC26000;

DT 18-DEC-2003 (first entry)

DE Human purinergic receptor P2Y-related GPCR α 6 protein.

XX virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
 XX anorectic; cardiant; hypotensive; osteopathic; antianginal;
 KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
 KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
 KW GPCR; viral; fungal; bacterial infection; immune-related disorder;
 KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
 KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
 KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;

KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
 KW human; GPCR α ; purinergic receptor P2Y.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 62
 FT /note= "Encoded by TTT"
 FT Misc-difference 243
 FT /note= "Encoded by AAG"

XX US2003088080-A1.

PD 08-MAY-2003.

XX 21-JUN-2001; 2001US-00885453.

XX 20-JUN-2000; 2000US-0212908P.

XX 05-DEC-2000; 2000EP-00870289.

XX (COMM/) COMMUNI D.

XX (LANW/) LANNOY V.

XX (GOVA/) GOVAERTS C.

XX (PARM/) PARMENTIER M.

XX (DETH/) DETHEUX M.

XX Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;

XX WPI; 2003-657983/62.

XX N-PSDB; ADC25999.

XX New human G-protein coupled receptor, useful for treating receptor-
 PT mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
 PT acute heart failure, osteoporosis, stroke, ulcer, allergy, or
 PT neurological disorders.

XX Example 3; Page 15-16; 24pp; English.

XX The invention relates to a novel G-protein coupled receptor (GPCR). The
 CC receptor, polynucleotide, agonist, reverse agonist and antagonist of the
 CC invention may be useful for treating receptor-mediated disorders
 CC including viral, fungal or bacterial infections, immune-related disorders
 CC such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
 CC hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
 CC ulcer and allergy, as well as psychotic and neurological disorders such
 CC as schizophrenia and dementia, degenerative diseases such as Parkinson's
 CC disease and Alzheimer's disease and dyskinesias such as Huntington's
 CC disease. The current sequence is that of the human purinergic receptor
 CC P2Y-related GPCR α 6 protein of the invention.

XX Sequence 338 AA;

Query Match 57.5%; Score 1041; DB 7; Length 338;
 Best Local Similarity 97.5%; Pred. No. 1e-105;
 Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKYDMNTSQOGLCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
 Db 29 MEKYDMNTSQOGLCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
 Qy 61 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCTISVHQ 120
 Db 89 YLVNLMWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCTISVHQ 148
 Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSEN 180
 Db 149 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSEN 208
 Qy 181 FDRLPFAYGIVLTLSGFLS 200
 Db 209 FDRLPFAYGIVLTLSGFLS 228

```

RESULT 13
ADC86167
ID  ADC86167 standard; protein; 271 AA.
XX
XX  AC  ADC86167;
XX
XX  DT  01-JAN-2004 (first entry)
XX
XX  DE  Human GPCR protein SEQ ID NO:620.
XX
XX  KW  human; GPCR; guanosine triphosphate-binding protein coupled receptor;
XX  KW  gene therapy.
XX
XX  OS  Homo sapiens.
XX
XX  PN  EP1270724-A2.
XX
XX  PD  02-JAN-2003.
XX
XX  PF  18-JUN-2002; 2002EP-00013517.
XX
XX  PR  18-JUN-2001; 2001JP-00246789.
XX
XX  PA  (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX  PA  (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX  PI  Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX  DR  WPI; 2003-315783/31.
XX
XX  DR  N-PSDB; ADC86166.
XX
XX  PS  Claim 2; SEQ ID NO 620; 28pp; English.
XX
XX  CC  The invention relates to a novel polynucleotide encoding a guanosine
XX  CC  triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX  CC  the invention may have a use in gene therapy. The polynucleotide and
XX  CC  polypeptide are useful for preparing a composition for treating a patient
XX  CC  in need of increased or suppressed activity or expression of the
XX  CC  guanosine triphosphate-binding protein coupled receptor. The protein
XX  CC  sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
XX  SQ  Sequence 271 AA;

Query Match          51.7%; Score 936; DB 7; Length 271;
Best Local Similarity 86.0%; Pred. No. 3e-94;
Matches 178; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy  1 MEKVDNMNTSQBGLCFSEKTKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db  1 MEKVDNMNTSQBGLCFSEKTKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Qy  61 YLVNLMVADLLYVLLPELLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120
Db  61 YLVNLMVADLLYVLLPELLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120
Qy  121 FLGVCHPLCSLPYTRRHAWLGTSTTVALVQLPLTAFSHSDTYINGQMIWDMTSQEN 180
Db  121 FLGVCHPLCSLPYTRRHAWLGTSTTVALVQLPLTAFSHSDTYINGQMIWDLIKPEEN 180
Qy  181 FDLRFAYGIVLTLSGFSLSLGHFGVLF 207
Db  181 LMRGTNTARARSIRTIILLVCLFLTLCF 207

RESULT 14
AAG80935
ID  AAG80935 standard; protein; 170 AA.
XX
XX  AC  AAG80935;

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XX  DT  28-AUG-2001 (first entry)
XX  DE  Human nGPCR12.
XX
XX  KW  G protein-coupled receptor; nGPCR; seven transmembrane receptor;
XX  KW  signal transduction; schizophrenia; thyroid disorder; renal failure;
XX  KW  rheumatoid arthritis; CNS disorder; infection; metabolic disease;
XX  KW  cardiovascular disease; proliferative disorder; hormonal disorder;
XX  KW  neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
XX  KW  attention deficit-hyperactivity disorder/attention deficit disorder;
XX  KW  Parkinson's disease; migraine; senile dementia; inflammatory disease;
XX  KW  rheumatoid arthritis; autoimmune disorder; respiratory ailment;
XX  KW  neuroprotective.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200136473-A2.
XX
XX  PD  25-MAY-2001.
XX
XX  PF  16-NOV-2000; 2000WO-US031581.
XX
XX  PR  16-NOV-1999; 99US-0165838P.
XX  PR  17-NOV-1999; 99US-0166071P.
XX  PR  19-NOV-1999; 99US-0166578P.
XX  PR  28-DEC-1999; 99US-0173396P.
XX  PR  22-FEB-2000; 2000US-0184129P.
XX  PR  28-FEB-2000; 2000US-0185421P.
XX  PR  28-FEB-2000; 2000US-0185554P.
XX  PR  02-MAR-2000; 2000US-0186530P.
XX  PR  03-MAR-2000; 2000US-0186811P.
XX  PR  09-MAR-2000; 2000US-0188114P.
XX  PR  17-MAR-2000; 2000US-0190310P.
XX  PR  21-MAR-2000; 2000US-0190800P.
XX  PR  20-APR-2000; 2000US-0198568P.
XX  PR  02-MAY-2000; 2000US-0201190P.
XX  PR  08-MAY-2000; 2000US-0203111P.
XX  PR  23-MAY-2000; 2000US-0207094P.
XX
XX  PA  (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX  PI  Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
XX  PI  Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX
XX  DR  WPI; 2001-389826/41.
XX  DR  N-PSDB; AAH50975.
XX
XX  PT  New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
XX  PT  useful for diagnosing and treating e.g. schizophrenia.
XX
XX  PS  Claim 37; Page 78; 261pp; English.
XX
XX  CC  The present invention relates to novel G protein-coupled receptors
XX  CC  (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
XX  CC  31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
XX  CC  one such G protein-coupled receptor. GPCRs are also known as seven
XX  CC  transmembrane receptors and function in signal transduction. The nGPCRx
XX  CC  coding sequences are useful for screening a human to diagnose a disorder
XX  CC  affecting the brain or a genetic predisposition, specifically
XX  CC  schizophrenia. nGPCRx are useful for identifying compounds useful for
XX  CC  treating schizophrenia. Detection of nGPCRx in a sample is useful as a
XX  CC  diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
XX  CC  failure, rheumatoid arthritis, CNS disorders, infectious such as HIV-1,
XX  CC  metabolic and cardiovascular diseases, proliferative disorders and
XX  CC  hormonal disorders. Modulators of nGPCRx activity have the utility for
XX  CC  treating neurological disorders, including schizophrenia, ADHD/ADD
XX  CC  (attention deficit-hyperactivity disorder/attention deficit disorder),
XX  CC  and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
XX  CC  migraine and senile dementia. Additional disorders include inflammatory
XX  CC  conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
XX  CC  disorders, cancers, respiratory ailments such as asthma, and inflammatory
XX  CC  diseases e.g. inflammatory bowel disease

```

```
XX SQ Sequence 170 AA;
Query Match 50.8%; Score 921; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFGLCKLVHFLFYINLYGSILLT 114
Db 1 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFGLCKLVHFLFYINLYGSILLT 60

Qy 115 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIWD 174
Db 61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIWD 120

Qy 175 MTSQENFDRLPAYGIVLTLSGLSLILGHFGVLTGQEPDQARGEPHEDR 224
Db 121 MTSQENFDRLPAYGIVLTLSGLSLILGHFGVLTGQEPDQARGEPHEDR 170

RESULT 15
ABG93753
ID ABG93753 standard; protein; 170 AA.
XX AC ABG93753;
XX DT 26-NOV-2002 (first entry)
XX DE Human G protein-coupled receptor protein, beGPCR-seq12.
XX KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
KW nG protein coupled receptor; communication; serpentine structure;
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW genetic predisposition; brain; immune response; gene therapy;
KW anxiety disorder; depression; bipolar disorder; schizophrenia;
KW Huntington's disease; dyskinesia; manic depression; stroke;
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW tranquiliser.
XX OS Homo sapiens.
XX FN WO200264789-A1.
XX PD 22-AUG-2002.
XX PP 14-FEB-2001; 2001WO-US004641.
XX PR 14-FEB-2001; 2001WO-US004641.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI Lind P, Parodi LA, Vogeli G, Wood LS;
XX DR WPI; 2002-674879/72.
XX DR N-PSDB; ABS70208.
XX PT New nucleic acids and polypeptides of the nG protein-coupled receptor,
XX useful for treating or diagnosing a mental disorder or a disorder
XX affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
XX Parkinson's disease.
XX PS Example 1; Page 73; 244pp; English.
XX CC The invention discloses an isolated human polypeptide, and encoding
XX nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
XX nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
XX communication between cells and their environment and are characterised
XX by a serpentine structure that passes through the cell membrane seven
XX times, hence the reason such receptors are sometimes called seven
XX transmembrane receptors (7TM). The polynucleotides and polypeptides are
XX useful for identifying an nGPCR allelic variant that correlates with a
XX mental disorder, for isolating an antibody that binds to an epitope of
XX the polypeptide, for identifying a compound that binds the polypeptide or
```

polynucleotide and/or modulates its biological activity, for screening a human subject to diagnose a disorder, or a genetic predisposition to a disorder, affecting the brain or a genetic disposition to the disorder, for identifying compounds useful for the treatment of a mental disorder, and for identifying a compound useful as a modulator of binding between nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also useful for inducing an immune response in a mammal. The nucleic acid or polypeptide is particularly useful, using gene therapy, for treating e.g. anxiety disorders, depression, bipolar disorder, schizophrenia, Huntington's disease, dyskinesia, manic depression, stroke, Parkinson's disease or Alzheimer's disease. The nucleic acid and polypeptide may also be used for treating diabetes, inflammation or wounds. The sequences presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also referred to as beGPCRs) proteins

XX SQ Sequence 170 AA;

Query Match 50.8%; Score 921; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 55 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFGLCKLVHFLFYINLYGSILLT 114
Db 1 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFGLCKLVHFLFYINLYGSILLT 60

Qy 115 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIWD 174
Db 61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIWD 120

Qy 175 MTSQENFDRLPAYGIVLTLSGLSLILGHFGVLTGQEPDQARGEPHEDR 224
Db 121 MTSQENFDRLPAYGIVLTLSGLSLILGHFGVLTGQEPDQARGEPHEDR 170
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Search completed: February 13, 2006, 14:38:20
Job time : 188 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:53:44 ; Search time 166 Seconds
(without alignment)
838.176 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

Sequence: 1 MEKVDNMTSQEQLGCFSEK.....NKLGEHPAGRKRCPLNRSG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA Main:
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1812	100.0	333	4	US-10-088-726-20
2	1798	99.2	360	4	US-10-023-586B-2
3	1798	99.2	360	4	US-10-763-972-2
4	1536	84.8	295	4	US-10-275-910-2
5	1397	77.1	361	4	US-10-072-012-166
6	1051	58.0	338	3	US-09-885-453-4
7	1047	57.8	339	4	US-10-079-384-6
8	1047	57.8	339	4	US-10-023-586B-4
9	1047	57.8	339	4	US-10-333-946-1
10	1047	57.8	339	4	US-10-763-972-4
11	936	51.7	271	4	US-10-017-161-708
12	936	51.7	271	4	US-10-292-798-620
13	921	50.8	170	3	US-09-782-974C-14
14	921	50.8	170	5	US-10-467-492A-14
15	921	50.8	170	5	US-10-975-979-14
16	921	50.8	170	5	US-10-969-727-14
17	449	24.8	328	4	US-10-010-568-10
18	449	24.8	328	4	US-10-010-568-14
19	449	24.9	328	4	US-10-275-910-3
20	449	24.8	328	4	US-10-375-157-10
21	449	24.8	328	4	US-10-375-157-14
22	449	24.8	328	4	US-10-072-012-519
23	449	24.8	328	4	US-10-072-012-520
24	429	23.7	374	3	US-09-745-842-15
25	429	23.7	374	4	US-10-010-568-11
26	429	23.7	374	4	US-10-375-157-11
27	429	23.7	374	4	US-10-072-012-518

28	424	23.4	537	4	US-10-311-956-4	Sequence 4, Appli
29	424	23.4	537	4	US-10-010-568-12	Sequence 12, Appl
30	424	23.4	537	4	US-10-375-157-12	Sequence 12, Appl
31	424	23.4	537	4	US-10-055-569A-52	Sequence 52, Appl
32	424	23.4	537	4	US-10-072-012-517	Sequence 517, App
33	397	21.9	328	4	US-10-278-087A-39	Sequence 39, Appl
34	396	21.9	361	3	US-09-964-821B-15	Sequence 15, Appl
35	396	21.9	361	4	US-10-010-568-9	Sequence 9, Appli
36	396	21.9	361	4	US-10-268-332-15	Sequence 15, Appli
37	396	21.9	361	4	US-10-375-157-9	Sequence 9, Appli
38	396	21.9	361	4	US-10-072-012-521	Sequence 521, App
39	396	21.9	361	4	US-10-775-965-15	Sequence 15, Appl
40	395.5	21.8	377	3	US-09-745-842-17	Sequence 17, Appl
41	395.5	21.8	377	4	US-10-225-567A-217	Sequence 217, App
42	395.5	21.8	377	5	US-10-756-149-5688	Sequence 5688, Ap
43	394.5	21.8	328	4	US-10-278-087A-56	Sequence 56, Appl
44	389.5	21.5	328	3	US-09-745-842-18	Sequence 18, Appl
45	389.5	21.5	328	4	US-10-225-567A-223	Sequence 223, App

ALIGNMENTS

RESULT 1

US-10-088-726-20
; Sequence 20, Application US/10088726
; Publication No: US20030157558A1

GENERAL INFORMATION:

; APPLICANT: Matsumoto et al.

; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AI
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088,726

; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: PCT/JP00/09408

; PRIOR FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: JP 1999-375152

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: JP 2000-101339

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-088-726-20

Query Match 100.0%; Score 1812; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.7e-162;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEKVDNMTSQEQLGCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFGQTKRWSCATT	60
Db	1	MEKVDNMTSQEQLGCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFGQTKRWSCATT	60
Qy	61	YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTTCISVHQ	120
Db	61	YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTTCISVHQ	120
Qy	121	FLGVCHPLCSLPYTRRRHAWLGTSTTWALVVLQLLPTLAFSHDTDYINGQMIWDMTSQEN	180
Db	121	FLGVCHPLCSLPYTRRRHAWLGTSTTWALVVLQLLPTLAFSHDTDYINGQMIWDMTSQEN	180
Qy	181	FDRLPAYGIVLTLSGFLSLGLHFGVLFDTGQEPQARGEPHEDRHQHSQVHPDHTGW	240
Db	181	FDRLPAYGIVLTLSGFLSLGLHFGVLFDTGQEPQARGEPHEDRHQHSQVHPDHTGW	240
Qy	241	PLHPLFCALPYHSLLLPHLLLSAFSGLPALDQSCGLQDMEASGECEQLPPSPVLSFGK	300
Db	241	PLHPLFCALPYHSLLLPHLLLSAFSGLPALDQSCGLQDMEASGECEQLPPSPVLSFGK	300
Qy	301	GKNRVRLQLKRNQKLGHPAGRKRCPLNRSG	333

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Db 301 GKNRVLQLKRLQKLGHPAGKRCPCGLNRS 333
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; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-763-972-2

Query Match 99.2%; Score 1798; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 4.1e-161;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db 29 MEKVDMTSQQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTTCISVHQ 120
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTTCISVHQ 148
Qy 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 180
Db 149 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
Qy 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTGQEPDQARGEPEHROHSPSOVHPDHPGTVW 240
Db 209 FDLRFAYGIVLTLSGFLSLGLHFGVLTGQEPDQARGEPEHROHSPSOVHPDHPGTVW 268
Qy 241 PLHPLFCALPYHSLLLPHLLSAFSGLPALDGSQGLQDMASGECEQLPQSPVLSFKG 300
Db 269 PLHPLFCALPYHSLLLPHLLSAFSGLPALDGSQGLQDMASGECEQLPQSPVLSFKG 328
Qy 301 GKNRVLQLKRLQKLGHPAGKRCPCGLNRS 332
Db 329 GKNRVLQLKRLQKLGHPAGKRCPCGLNRS 360

RESULT 4
US-10-275-910-2
; Sequence 2, Application US/10275910
; Publication No. US20030166142A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 4974.00885
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 60/203,582
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/269,857
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-275-910-2

Query Match 84.8%; Score 1536; DB 4; Length 295;
Best Local Similarity 98.3%; Pred. No. 1.8e-136;
Matches 283; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db 1 MEKVDMTSQQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
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QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 120
Db 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 120
QY 121 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWDMTSQEN 180
Db 121 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWDMTSQEN 180
QY 181 FDRLFAYGIVLTLSGFLSLHGHFVLTGQGPDOARGEPEHEDRQHSQVHPDHPPTGVW 240
Db 181 FDRLFAYGIVLTLSGFLSLHGHFVLTGQGPDOARGEPEHEDRQHSQVHPDHPPTGVW 240
QY 241 PLHPLFCALPYHSLLLPHHLLSAPGLPALDGSQCGLQDMEASGCEQ 288
Db 241 PLHPLFCALPYHSLLLPHHLLSAPGLPALDGSQCGLQDMEASGCEQ 288
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RESULT 5

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US-10-072-012-166
; Sequence 166, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shamketa, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir V.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072, 012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 166
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-166
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Query Match 77.1%; Score 1397; DB 4; Length 361;
Best Local Similarity 80.9%; Pred. No. 3.1e-123;
Matches 275; Conservative 11; Mismatches 40; Indels 14; Gaps 5;
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QY 1 MEKVDMTSQSGLCQFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60
Db 29 MEKVDMTSQSGLCQFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88
QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 120
Db 89 YLVNLMVADLLVLLPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 148
QY 121 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWDMTSQEN 180
Db 149 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWDMTSQEN 208
QY 181 FDRLFAYGIVLTLSGFLSLHGHFVLTGQGPDOARGEPEHEDRQHSQVHPDHPPTG 238
Db 209 FDRLFAYGIVLTLSGFLSLHGHFVLTGQGPDOARGEPEHEDRQHSQVHPDHPPTG 262
QY 239 VWPLHPLF--CALPYHSLLLPHHLLSAP---SGLPALDGSQCGLQDMEASGCEQ 293
Db 263 ILLVCGLTCLFVPPH-ITRSFYLTICFLLSQDCQLLMAAQCGLQDMEASGCEQ 321
QY 294 PVLGFKGKGNRVRLQLKRNKLGEHPAGRKRCPCGLNRSG 333
Db 322 PVLGFKGKGNRVRLQLKRNKLGEHPAGRKRCPCGLNRSG 361
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RESULT 6

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US-09-885-453-4
; Sequence 4, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCRxi10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Amino acid sequence
; LOCATION: (1)..(338)
; OTHER INFORMATION: GPCRxi6 amino acid sequence
US-09-885-453-4
```

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Query Match 58.0%; Score 1051; DB 3; Length 338;
Best Local Similarity 98.0%; Pred. No. 1.4e-90;
Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 MEKVDMTSQSGLCQFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60
Db 29 MEKVDMTSQSGLCQFSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88
QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 120
Db 89 YLVNLMVADLLVLLPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 148
QY 121 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWDMTSQEN 180
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Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208
Qy      181 FDRLFAYGIVLTLSGFLSL 200
      |||||
Db      209 FDRLFAYGIVLTLSGFFPSL 228

RESULT 7
US-10-079-384-6
; Sequence 6, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communis, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-6

Query Match      58.0%; Score 1051; DB 4; Length 338;
Best Local Similarity 98.0%; Pred. No. 1.4e-90;
Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 MEKVDNMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
      |||||
Db      29 MEKVDNMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88

Qy      61 YLVNLMVADLLVLLPLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTLCISVHQ 120
      |||||
Db      89 YLVNLMVADLLVLLPLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTLCISVHQ 148

Qy      121 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180
      |||||
Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208

Qy      181 FDRLFAYGIVLTLSGFLSL 200
      |||||
Db      209 FDRLFAYGIVLTLSGFFPSL 228

RESULT 8
US-10-023-586B-4
; Sequence 4, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (EP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US20030166882A1el Polypeptide
; FILE REFERENCE: PC10960AGR
; CURRENT APPLICATION NUMBER: US/10/023,586B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 339
; TYPE: PRT

Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208
Qy      181 FDRLFAYGIVLTLSGFLSL 200
      |||||
Db      209 FDRLFAYGIVLTLSGFFPSL 228

RESULT 9
US-10-333-946-1
; Sequence 1, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CD1
US-10-333-946-1

Query Match      57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; ORGANISM: Homo sapiens
US-10-023-586B-4

Query Match      57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MEKVDNMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
      |||||
Db      29 MEKVDNMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88

Qy      61 YLVNLMVADLLVLLPLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTLCISVHQ 120
      |||||
Db      89 YLVNLMVADLLVLLPLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTLCISVHQ 148

Qy      121 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180
      |||||
Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208

Qy      181 FDRLFAYGIVLTLSGFLSL 198
      |||||
Db      209 FDRLFAYGIVLTLSGFLSL 226
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RESULT 9
US-10-333-946-1
; Sequence 1, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CD1
US-10-333-946-1

Query Match      57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
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Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
Db 29 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 88
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 148
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 180
Db 149 FLGVWHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
Qy 181 FDLRFAYGIVLTLSGFLS 198
Db 209 FDLRFAYGIVLTLSGFLS 226

RESULT 10
US-10-763-972-4
; Sequence 4, Application US/10763972
; Publication No. US20040137500A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER INC.
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10960B
; CURRENT APPLICATION NUMBER: US/10763,972
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-763-972-4

Query Match 57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
Db 29 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 88
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 148
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 180
Db 149 FLGVWHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
Qy 181 FDLRFAYGIVLTLSGFLS 198
Db 209 FDLRFAYGIVLTLSGFLS 226

RESULT 11
US-10-017-161-708
; Sequence 708, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO

; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 708
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-708

Query Match 51.7%; Score 936; DB 4; Length 271;
Best Local Similarity 86.0%; Pred. No. 7.9e-80;
Matches 178; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
Db 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120
Db 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 180
Db 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 180
Qy 181 FDLRFAYGIVLTLSGFLSILGHFGVLF 207
Db 181 LMRGTARARSIRINTILLVCGFLTLCF 207

RESULT 12
US-10-292-798-620
; Sequence 620, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 620
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-620

Query Match 51.7%; Score 936; DB 4; Length 271;
Best Local Similarity 86.0%; Pred. No. 7.9e-80;
Matches 178; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
Db 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKWSCATT 60
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120

Db 61 YLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSILLTTCISVHQ 120
Qy 121 FLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSOEN 180
Db 121 FLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWLIKPEEN 180
Cy 181 FDRLFAYGIVLTLSGFLSLGLGHFGVLF 207
Db 181 LMRTGNTARARSIRTIILLVCGFLTLCP 207

RESULT 13

US-09-782-974C-14
; Sequence 14, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: Novel G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-782-974C-14

Query Match 50.8%; Score 921; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.le-78;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 55 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSILLT 114
Db 1 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSILLT 60
Qy 115 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 174
Db 61 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 120
Qy 175 MTSQENFDRLPAYGIVLTLSGFLSLGLGHFGVLFDTGQEPDQARGEPEHEDR 224
Db 121 MTSQENFDRLPAYGIVLTLSGFLSLGLGHFGVLFDTGQEPDQARGEPEHEDR 170

RESULT 14

US-10-467-492A-14
; Sequence 14, Application US/10467492A

; Publication No. US20050069976A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn Company
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: Novel G Protein Coupled Receptor
; FILE REFERENCE: 0411PFRM313
; CURRENT APPLICATION NUMBER: US/10/467,492A
; CURRENT FILING DATE: 2003-08-07
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-467-492A-14

Query Match 50.8%; Score 921; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.le-78;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 55 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSILLT 114
Db 1 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSILLT 60
Qy 115 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 174
Db 61 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 120
Qy 175 MTSQENFDRLPAYGIVLTLSGFLSLGLGHFGVLFDTGQEPDQARGEPEHEDR 224
Db 121 MTSQENFDRLPAYGIVLTLSGFLSLGLGHFGVLFDTGQEPDQARGEPEHEDR 170

RESULT 15

US-10-975-979-14
; Sequence 14, Application US/10975979
; Publication No. US20050112660A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Huff, Rita
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Lind, Peter
; APPLICANT: Slightom, Jerry
; APPLICANT: Schellin, Kathleen
; APPLICANT: Bannigan, Chris
; APPLICANT: Ruff, Valerie
; APPLICANT: Kaytes, Paul
; APPLICANT: Wood, Linda
; APPLICANT: Parodi, Luis
; APPLICANT: Hiebsch, Ronald
; TITLE OF INVENTION: Novel G Protein Coupled Receptors
; FILE REFERENCE: 00431PFRM293
; CURRENT APPLICATION NUMBER: US/10/975,979
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28

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; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-979-14

Query Match      50.8%; Score 921; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.1e-78;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55  WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFPGELCKLVHFLFYINLYGSILLT 114
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Db      1  WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFPGELCKLVHFLFYINLYGSILLT 60

Qy      115  CISVHQFLGVCVCHPLCSLPYRTRRHAWLGTSTWALVVLQLLPTLAFSHTDYINGQMIWYD 174
          |||||||
Db      61  CISVHQFLGVCVCHPLCSLPYRTRRHAWLGTSTWALVVLQLLPTLAFSHTDYINGQMIWYD 120

Qy      175  MTSQENFDRLPAYGIVLTLGFLSLGHFGVLTGQSPDQARGEPEHEDR 224
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Db      121  MTSQENFDRLPAYGIVLTLGFLSLGHFGVLTGQSPDQARGEPEHEDR 170
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Search completed: February 13, 2006, 14:56:58
Job time : 167 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 14:54:19 ; Search time 16 Seconds
(without alignments)
273.113 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

Sequence: 1 MEKVDNMTSQSGQLCQFSEK.....NKLGEHPAGKRCPLNRSRG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

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- 2: /cgn2_6/ptodata/2/pubpaa/US06 NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07 NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09 NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10 NEW_PUB.pap.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11 NEW_PUB.pap.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60 NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	375	20.7	365	6	US-10-995-561-545
2	336	18.5	373	7	US-11-127-877-46
3	257	14.2	339	7	US-11-157-930-4
4	257	14.2	367	7	US-11-157-930-6
5	247	13.6	388	6	US-10-995-561-713
6	247	13.6	394	6	US-10-995-561-714
7	247	13.6	394	6	US-10-995-561-715
8	244	13.5	359	6	US-10-995-561-712
9	244	13.5	359	6	US-10-995-561-716
10	244	13.5	359	6	US-11-127-877-65
11	243.5	13.4	359	6	US-10-876-787-2
12	238	13.1	97	6	US-10-980-388-92
13	234.5	12.9	485	6	US-10-821-234-934
14	227.5	12.6	254	6	US-10-055-877-248
15	227.5	12.6	254	6	US-10-055-877-327
16	227.5	12.6	254	6	US-10-055-877-340
17	227.5	12.6	254	6	US-10-877-346-83
18	226.5	12.5	346	7	US-11-157-930-2
19	224	12.4	349	7	US-11-028-922A-2
20	224	12.4	371	7	US-11-134-811-4
21	224	12.4	371	7	US-11-218-281-2
22	224	12.4	371	7	US-11-218-281-33
23	221.5	12.2	269	7	US-11-151-482-5
24	221.5	12.2	333	7	US-11-127-877-57
25	220.5	12.2	355	7	US-11-218-281-26

26	220	12.1	400	7	US-11-127-877-55	Sequence 55, Appl
27	218	12.0	371	7	US-11-134-811-6	Sequence 6, Appl
28	218	12.0	371	7	US-11-218-281-3	Sequence 3, Appl
29	217.5	12.0	351	7	US-11-218-281-12	Sequence 12, Appl
30	217.5	12.0	351	7	US-11-218-281-24	Sequence 24, Appl
31	216	11.9	375	7	US-11-127-877-67	Sequence 67, Appl
32	214	11.8	360	6	US-10-959-310-36	Sequence 36, Appl
33	210.5	11.6	371	7	US-11-134-811-2	Sequence 2, Appl
34	210.5	11.6	373	7	US-11-218-281-1	Sequence 1, Appl
35	210.5	11.6	373	7	US-11-218-281-28	Sequence 28, Appl
36	206.5	11.4	352	7	US-11-028-922A-1	Sequence 1, Appl
37	206	11.4	353	7	US-11-218-281-25	Sequence 25, Appl
38	205	11.3	337	7	US-11-166-412-60	Sequence 60, Appl
39	203.5	11.2	259	6	US-10-055-877-225	Sequence 225, App
40	203.5	11.2	259	6	US-10-055-877-237	Sequence 237, App
41	203.5	11.2	482	7	US-11-169-976-2	Sequence 2, Appl
42	203.5	11.2	482	7	US-11-218-281-30	Sequence 30, Appl
43	202.5	11.2	415	7	US-11-017-058-2	Sequence 2, Appl
44	201.5	11.1	353	7	US-11-017-058-9	Sequence 9, Appl
45	200.5	11.1	350	6	US-10-502-145-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-995-561-545
; Sequence 545, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-545

Query Match 20.7%; Score 375; DB 6; Length 365;
Best Local Similarity 41.7%; Pred. No. 1.3e-26;
Matches 80; Conservative 30; Mismatches 74; Indels 8; Gaps 3;

Qy	15	CQFSEKYQVYLSAYSIIFILGLPLNGTGLVHFWGQTKRWCATTYLVNLMVADLLVYL	74
Db	27	CWFDEDFKILLPVSYAVVFLGGLNAPTULWLFIFLRUPWDATATYMFHLSDTLVL	86
Qy	75	-LPFLITYSLDDRRPFGEELCKLVHFLFYINLYCSILLTLCISVHQPLGVCHPLCSLPY	133
Db	87	SLPTLIYYAAHNPFGTEICKFVFLFYWNLYCSVLFLTCISVHRYLGICHLRALRW	146
Qy	134	RTRHAMIGTSTTVALVVLQLLPTLASHTDYINGQMIWYDNTSOENFDRLFAYGIVITL	193
Db	147	GRPRLAGLLCLAVLWVAGCLVPNLFVFTTSNKGTTVLCHDTRREEDFDYHFS----	201
Qy	194	SGFLSLICHGVQ	205
Db	202	SAVNGLL--FGV	211

RESULT 2

US-11-127-877-46
; Sequence 46, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel

APPLICANT: Spittäels, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
FILE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: PatentIn version 3.3
SEQ ID NO 46
LENGTH: 373
TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-877-46

Query Match 18.5%; Score 336; DB 7; Length 373;
Best Local Similarity 30.2%; Pred. No. 4.4e-23;
Matches 94; Conservative 51; Mismatches 122; Indels 44; Gaps 10;
QY 25 YLSLAYSIFILGLPLNGTVLWHFWGQTKRWSGATTVLVNLMVADLLVYL-LPELIITYS 83
DB 53 YLPVAVILVFIIGFGLGNSVAIWMFVFMKPMGSGISVTMENALADFLVLTLPALIFYF 112
QY 84 LDDRPFGELCKLVHFLFYINLYGSIILLTICISVHQFLGVCHPLCSLPYRTRHAWLGT 143
DB 113 NKTDWIFGDAMCKLQRFIFHVNLYGSIILFTICISAHRYSGVVYPLKSLGRLLKKNACIS 172
QY 144 STWALVVLQLLPTLAFSHDTYINGQMI-WYDWTSGNQENFRLFAIGVILVLSGF----LS 198
DB 173 VLVWLIWVAISPILFYSGTGRVKNKTICTYDTSDEYLSRYFYISMCTTVAMFCVPLVL 232
QY 199 LLGHFGLVLTGQDQEPQARGPHEPDROHSPSOVHPDPTGWPPLHPLFCALPYHSL-LLP 257
DB 233 ILGCYGLI-----VRALIYKLDLNSPURK-----SYLVIIIVTVFAVSYIP 275
QY 258 HHLISAFSGPLALD---GSCGLQD-----MEASGECPQLPQSPVLSFKGGKN 303
DB 276 FHVMTWNLRLARLDQTPAMCAFNDRVVATYQVTRGLASLNSC-----VDPILVFLAGDT 330
QY 304 -RVLLQKLKQ 313
DB 331 FRRLSRATRK 341

RESULT 3
US-11-157-930-4
Sequence 4, Application US/11157930
Publication No. US20050266482A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
FILE REFERENCE: 04974.00458
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-11-157-930-4

Query Match 14.2%; Score 257; DB 7; Length 339;
Best Local Similarity 33.0%; Pred. No. 5.2e-16;
Matches 59; Conservative 34; Mismatches 78; Indels 8; Gaps 2;
QY 30 YSIIFILGLPLNGTVLWHFWGQTKRWSGATTVLVNLMVADLLVYL-LPELIITYSLDDRW 88
DB 38 YLLDFILALVGNLTALWLFI RDHKS GTPANVFLMHLAVADLSCVLVLPTRLVYHFSGNHW 97
QY 89 PGFELCKLVHFLFYINLYGSIILLTICISVHQFLGVCHPLCSLPYRTRHAWLGTSTWA 148
DB 98 PFGEIACRLTGFLFYLMNVASIFYELTICISADRELAIVHPVKSLKRLRPLVAHLACAFWV 157
QY 149 LVVLQLLPTLAFSHDTYINGQMIWYDWTSGE-----NFDRLFAYGIVLTLSGFLSLL 200
DB 158 VVAVAMAPLLVSPQTQVNTHTVVVQLQLYREKASHALVSLAVAFPTFPFITVTCYLLII 216

RESULT 4
US-11-157-930-6
Sequence 6, Application US/11157930
Publication No. US20050266482A1
GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
FILE REFERENCE: 04974.00458
CURRENT APPLICATION NUMBER: US/11/157,930
CURRENT FILING DATE: 2005-06-22
PRIOR APPLICATION NUMBER: US/09/828,478
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 367
TYPE: PRT
ORGANISM: Homo sapiens
US-11-157-930-6

Query Match 14.2%; Score 257; DB 7; Length 367;
Best Local Similarity 33.0%; Pred. No. 5.7e-16;
Matches 59; Conservative 34; Mismatches 78; Indels 8; Gaps 2;
QY 30 YSIIFILGLPLNGTVLWHFWGQTKRWSGATTVLVNLMVADLLVYL-LPELIITYSLDDRW 88
DB 66 YLLDFILALVGNLTALWLFI RDHKS GTPANVFLMHLAVADLSCVLVLPTRLVYHFSGNHW 125
QY 89 PGFELCKLVHFLFYINLYGSIILLTICISVHQFLGVCHPLCSLPYRTRHAWLGTSTWA 148
DB 126 PFGEIACRLTGFLFYLMNVASIFYELTICISADRELAIVHPVKSLKRLRPLVAHLACAFWV 185
QY 149 LVVLQLLPTLAFSHDTYINGQMIWYDWTSGE-----NFDRLFAYGIVLTLSGFLSLL 200
DB 186 VVAVAMAPLLVSPQTQVNTHTVVVQLQLYREKASHALVSLAVAFPTFPFITVTCYLLII 244

RESULT 5
US-10-995-561-713
Sequence 713, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0

, PRIOR FILING DATE: 2001-03-14
 : Remaining Prior Application data removed - See File Wrapper or PALM.

GenCore version 5.1.7
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OM protein - protein search, using sw model

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598.500 Million cell updates/sec

Title: US-10-088-726-20
Perfect score: 1812
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	429	23.7	374	2	US-09-745-842-15
2	397	21.9	328	2	US-08-513-974B-39
3	397	21.9	328	2	US-08-513-974B-371
4	397	21.9	328	2	US-09-461-436B-39
5	395.5	21.8	377	2	US-09-745-842-17
6	394.5	21.8	328	2	US-08-513-974B-56
7	394.5	21.8	328	2	US-08-513-974B-380
8	394.5	21.8	328	2	US-09-461-436B-56
9	389.5	21.5	328	2	US-08-745-842-18
10	385.5	21.3	327	2	US-08-513-974B-372
11	382.5	21.1	375	1	US-08-442-134A-2
12	382.5	21.1	375	1	US-08-444-581B-2
13	382.5	21.1	375	1	US-08-446-088A-2
14	382.5	21.1	375	1	US-08-559-524A-3
15	382.5	21.1	375	2	US-08-749-707-3
16	382.5	21.1	375	2	US-09-947-922-3
17	377	20.8	373	2	US-08-513-974B-373
18	375	20.7	365	2	US-09-745-842-16
19	375	20.7	365	2	US-09-077-173D-2
20	372.5	20.6	374	2	US-09-102-710B-3
21	370.5	20.4	328	2	US-08-459-046-2
22	370.5	20.4	328	2	US-09-102-710B-2
23	348	19.2	362	2	US-08-513-974B-374
24	336	18.5	373	2	US-09-745-842-14
25	334.5	18.5	373	1	US-08-559-524A-4
26	334.5	18.5	373	2	US-08-749-707-4
27	334.5	18.5	373	2	US-09-947-922-4

28	283.5	15.6	337	2	US-10-314-048A-28	Sequence 28, Appl
29	282.5	15.6	302	1	US-08-467-948A-30	Sequence 30, Appl
30	282.5	15.6	302	2	US-08-467-947A-30	Sequence 30, Appl
31	281.5	15.5	344	1	US-08-467-948A-8	Sequence 8, Appl
32	281.5	15.5	344	2	US-08-467-947A-8	Sequence 8, Appl
33	263.5	14.5	370	2	US-08-781-250-2	Sequence 2, Appl
34	257	14.2	339	1	US-08-153-848-44	Sequence 44, Appl
35	257	14.2	339	1	US-08-812-871-3	Sequence 3, Appl
36	257	14.2	339	2	US-09-299-843A-44	Sequence 44, Appl
37	257	14.2	339	2	US-09-088-337B-44	Sequence 44, Appl
38	257	14.2	339	2	US-09-170-496D-32	Sequence 32, Appl
39	257	14.2	339	2	US-09-170-496D-182	Sequence 182, App
40	257	14.2	339	4	PCT-US93-11153-44	Sequence 44, Appl
41	257	14.2	339	4	PCT-US95-07180-2	Sequence 2, Appl
42	254	14.0	395	1	US-08-097-938-2	Sequence 2, Appl
43	254	14.0	395	1	US-08-097-938-5	Sequence 5, Appl
44	254	14.0	395	1	US-08-476-000-2	Sequence 2, Appl
45	254	14.0	395	1	US-08-476-000-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-745-842-15
; Sequence 15, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius David
; APPLICANT: Hollopetter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
; FEATURE:
; OTHER INFORMATION: Turkey P2Y nucleotide receptor; tp2ynovel
US-09-745-842-15

Query Match	23.7%	Score 429;	DB 2;	Length 374;
Best Local Similarity	40.8%;	Pred. No. 2.2e-30;		
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Db	26	TAAEAKCVNEEFKILLPISYGIVFVGGLPLNSWAWIFVSRMRPNWATTYMFNLAI 85		
Oy	68	ADLYVL-LPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLLCISVHQPLGVCH 126		
Db	86	SDTLVFSLEPLVYVYADRNWPFQVKVIFLVANLYSSILFLTCISVHRVWGICH 145		
Oy	127	PLCSLPYRTRHMLGTSTTVALVQLPLTASHTDYINGQMTWYDTSQENFDRLFA 186		
Db	146	FIRSLKWKTKHARLICVGVWLVTICLIPNLIFVTTSSKONSTLCHDTTKPEEFDHYH 205		
Oy	187	YGIVLTLSGFLSLGHFGVLF 207		
Db	206	YS-----SSIMALL--FGIPP 219		

RESULT 2
US-08-513-974B-39

APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 371:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-974B-371

Query Match 21.9%; Score 397; DB 2; Length 328;
Best Local Similarity 31.9%; Pred. No. 1.4e-27;
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;
Qy 1 MEKVDMTSQBGL----CFSEKVKQVYLSLAYSIIFILGPLNGTVLHFWGQTKRWS 56
Db 1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVSVLVGLPLNICVIAICASRRLLT 59
Qy 57 CATTYLVNLMVADLLYL-LPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSILLTC 115
Db 60 RSAVYTLNLADLMYACSLPLLIYNYARGDHPGDLACRFVRFLFYANLHGSILFLTC 119
Qy 116 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTVALVVLQLPTLAFSHTDYINGOMIWD 174
Db 120 ISFORYLGICHLASWHKRGERRAAWVGVVWLVAVTAQCLPTAVFAATGQRNRTVCYD 179
Qy 175 MTSQENFRLFAYGIVLTSLGFL----SLGHFGVLTDDGEPDOARGEHEDRHSQSQ 230
Db 180 LSPPLSTRYLPYGNALYVIGLFPFIALACYCMARRLCRQDGPAGVQAQRSSKAR 239
Qy 231 VHPDHTGVWPLHPLFCALPYHSLLLPHLL-SAFSGLPALDGGQCGLODMEASGECEQL 289
Db 240 M-----AVVAAVFAISLPHITKTAYLAVRSTPGVSCPVLFTFAAAYKGR 287
Qy 290 PQPS-----PVLSF-----KGGKRVRLLOKL 311
Db 288 PFASVNSVLDPLILFYFTQOKFRQPHDLQL 319

RESULT 4
US-09-461-436B-39
Sequence 39, Application US/09461436B
Patent No. 6538107
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma

Yasuaki Ito
Ryo Fujii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angell, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
FILING DATE: 19-APR-1995
APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
APPLICATION NUMBER: 7-007177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: <Unknown>
REFERENCE/DOCKET NUMBER: 45753 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
TELEFAX: 617-439-4170
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-461-436B-39

Query Match 21.9%; Score 397; DB 2; Length 328;
Best Local Similarity 31.9%; Pred. No. 1.4e-27;
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;
Qy 1 MEKVDMTSQBGL----CFSEKVKQVYLSLAYSIIFILGPLNGTVLHFWGQTKRWS 56
Db 1 MEQ-DNGTIQAPGLPPTTCVYREDFKRLLLTPVSVLVGLPLNICVIAICASRRLLT 59
Qy 57 CATTYLVNLMVADLLYL-LPFLIITYSLDDRWPFGLLCKLVHFLFYINLYGSILLTC 115

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Db 60 R5AVYTLNLAADLMYACSLPLLIIYNYARGDHPFGDLACRFVRFLEYANLHGSILFLTC 119
Qy 116 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGQMTIWD 174
Db 120 ISFORYLIGICHPLASMKRGRRAAWVCGVWMLAVTAQCLPTAVFAATG1QRNRTVCYD 179
Qy 175 MTSQENDRFLPAYGIVLTLSGFL-----SLLGHFGVLTGDQEPDQARGEPEHEDRQHSQ 230
Db 180 LSPILSTRYLPYGMATLVIGFLPFIALACYCRMARRLCRQDPGAPVQAQRRSAAAR 239
Qy 231 VHPDHPGVMPLHPLFCALPYHSLLLPHLL-SAFSGLPALDGSQCGLQDMEASGECEQL 289
Db 240 M-----AVVAAVFAISFLPHITKTAYLAVRSTPGVSCPVLETFAAAYKGR 287
Qy 290 PQPS-----PVLGSF-----KGGKNRVRLLQKL 311
Db 288 PFASVNSVLDPILFYFTQOKPRRQPHDLLQRL 319

RESULT 5
US-09-745-842-17
; Sequence 17, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-Dubridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopetter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P2Y2 purinergic receptor; p2ur
US-09-745-842-17

Query Match 21.8%; Score 395.5; DB 2; Length 377;
Best Local Similarity 33.0%; Pred. No. 2.2e-27;
Matches 118; Conservative 41; Mismatches 118; Indels 81; Gaps 13;

Qy 15 CQSEKTKQVLSIAYSIIFILGPLNGTVLWHPWGQTKRWSGATTVLNMVADLLYL 74
Db 25 CRFNEDEKYLPLVSVGYGVVGLCLNAVALYIFLCRLKTWNASTTYMFHLAVSDALYAA 84
Qy 75 -LPELITYSLDDRWPEGLLCKLAVHLYFYNLNGSILLTTCISVHQFLGVCHPLCSLPY 133
Db 85 SLPLLVYYARGDHWPFVTLCKLVRFLYTLNLYCSILFTLCISVHRCGLVRLRLRW 144
Qy 134 RTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGQMTIWDMTSQENFDRFLPAYGIVLTL 193
Db 145 GRARYARVAGAVVWVLACQAPVLYFVTTISARGRVTCHTDSAPELFSRFVAYSSVM-- 202
Qy 194 SGFLSLGHFGVLF-----TDGQEPDQARGEPEHEDRQHSQVHP 233
Db 203 ---LGLL--FAVPEAVILVCVLMARLLKPAYTSG-----GLPRAKRKSVRT--- 246
Qy 234 DHPTGVWPLHPLF--CALPYH-----SLLPLPHLLSAPS-----GLPALDGSQCQ 276
Db 247 -----IAVLAVFALCFPLPHVTHTLYSFRSLDSCHTLNAINMAYKVRPLASANS- 300
Qy 277 LQDMEASGECEQLPQPSFVLSFKGKNRVRLLQKLQNKLGHPA--GRKRCPCGLNRS 332
Db 301 -----LDPVLYFLAGRLVRFARDAKP-PTGPSPATPARRL-GLRS 341
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```
RESULT 6
US-08-513-974B-56
; Sequence 56, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 56:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-56

Query Match          21.8%; Score 394.5; DB 2; Length 328;
Best Local Similarity 33.0%; Pred. No. 2.3e-27;
Matches 109; Conservative 42; Mismatches 142; Indels 37; Gaps 9;

Qy 5 DMNTSQEQL-----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLMHFWGQTKRWSATT 60
Db 4 DNGTQALGLPPTTCVYRENFKQLLPVYSAVLAAGLPINICVITQICTSRALTRAV 63

Qy 61 YLVNLMVADLLYL-LPFLIITYSLDDRWPPGELLCKLVHFLFYINLYGSILLTCTISVH 119
Db :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
64 YTLNALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRELFYANLHGSILFLTCISFQ 123

Qy 120 QFLGVCHPLCSLPYR-TRRHAWLGTSITTWALVVLQLLPTLAFSHTDYINGQM1WYDMTSQ 178
Db :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
124 RYLGIChPLAPWHRKGGRRRAWLVCVTWLVAVTTQCLPTAIFATGIQRNRTVCYDLSP 183

Qy 179 ENFDRLPAYGIVLTLSGFL-----SLLGHFGLVFTDGOBPDQARGEPHEDROHSQVHPD 234
Db :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
184 ALATHYMPYGWALTIVIGFLLPFAALLACYCLAC-----RLCRDGGPAEPVAQ 231

Qy 235 HPTGVWPLHPLFCALPYHSLLLPHLL-SAFSGLPALDGSQGLQDMBASGECEQLPOP- 292
Db :||:||||| :||:||||| :||:||||| :||:||||| :||:||||| :||:|||||
232 ERRGKAARMVAVVAFAISFLPHITKTAYLAVGSTPGVCTV--LEAFAAAYKGRPF 289

Qy 293 -----SPVLSF-----KGGKNRVRLLOKL 311
Db ASANSVLDPILFYFTQKKFRRRPHELLLOKL 319

RESULT 7
US-08-513-974B-380
; Sequence 380, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinzuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ontaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
```



```
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 375 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-442-134A-2
;
; Query Match      21.1%; Score 382.5; DB 1; Length 375;
; Best Local Similarity 33.0%; Pred. No. 3.2e-26;
; Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;
;
QY 15 CQSEKVKQVYLSLAYSIIFILGILPLNGTVLWHFWGQTKWSCATTYLVNLMVADLLIYVL 74
DB 25 CRNFEDFKYLLPVSYGVWCVLGCLNAVGLYIFLCRLKTNWASTTYMFHLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSILLTLCISVHOFGLGVCHPLCSLPY 133
DB 85 SLPLLVYYARGDHWPFSTVLCKLVRFYTNLYCSILFLTCISVHRCGLGVRLRSLRW 144
QY 134 RTRHAWLGSTTVALVQLPLTAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 193
DB 145 GRARYARRVAGAVWVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLLGHGCVLF-----TDQEPDQARGEHEDRQHSQVHP 233
DB 202 ---LGLL--FAVPFAVILVCYLMARLLKPAYTSG-----GLPRAKRKSVRT--- 245
QY 234 DHPTGVNPLPLF--CALPYH-----SLLPHHLISAFSGLPALDGSQGLQDME 281
DB 246 -----IAVLAVALFALCFPHVTVRTLYYSRSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPOPSVLSFKGKGNRVRLQLKRONKLGHEHPA-GRKRCPLNRS 332
DB 294 SANSC-----LDPVLYFLAGQLRVRFARDAKP-PTGSPATPARRTLGLRRS 339

RESULT 12
US-08-444-581B-2
; Sequence 2, Application US/08444581B
; Patent No. 5607836
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5607836th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,581B
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/442,134
; FILING DATE: 16-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.

;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 375 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-442-134A-2
;
; Query Match      21.1%; Score 382.5; DB 1; Length 375;
; Best Local Similarity 33.0%; Pred. No. 3.2e-26;
; Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;
;
QY 15 CQSEKVKQVYLSLAYSIIFILGILPLNGTVLWHFWGQTKWSCATTYLVNLMVADLLIYVL 74
DB 25 CRNFEDFKYLLPVSYGVWCVLGCLNAVGLYIFLCRLKTNWASTTYMFHLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSILLTLCISVHOFGLGVCHPLCSLPY 133
DB 85 SLPLLVYYARGDHWPFSTVLCKLVRFYTNLYCSILFLTCISVHRCGLGVRLRSLRW 144
QY 134 RTRHAWLGSTTVALVQLPLTAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 193
DB 145 GRARYARRVAGAVWVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLLGHGCVLF-----TDQEPDQARGEHEDRQHSQVHP 233
DB 202 ---LGLL--FAVPFAVILVCYLMARLLKPAYTSG-----GLPRAKRKSVRT--- 245
QY 234 DHPTGVNPLPLF--CALPYH-----SLLPHHLISAFSGLPALDGSQGLQDME 281
DB 246 -----IAVLAVALFALCFPHVTVRTLYYSRSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPOPSVLSFKGKGNRVRLQLKRONKLGHEHPA-GRKRCPLNRS 332
DB 294 SANSC-----LDPVLYFLAGQLRVRFARDAKP-PTGSPATPARRTLGLRRS 339

RESULT 13
US-08-446-088A-2
; Sequence 2, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691156th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,088A
; FILING DATE: 19-MAY-1995
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-088A-2

Query Match      21.1%; Score 382.5; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

QY 15 CQSEKYYQVYLSLAYSIIIFILGLPLNGTVLWHFQGTKRWSCATTYLVNLMVADLLYVL 74
Db 25 CRFNEDFYVLLPVSYGVVGVLCGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQFLGVCHPLCSLPY 133
Db 85 SLPLLVYYARGDHPFSTVLCKLVRFYFNLYCSILFLTCTISVHRCGLGVLRPLRSRW 144
QY 134 RTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSONENFDRLFYAGIVLTL 193
Db 145 GRARYARRVAGAVVVLACQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLGHFGVLF-----TDGQEPDQARGEHPEDRQHSQVHP 233
Db 202 ---LGLL---FAVPAVILVCVLMARLLKPAYGTSG-----GLPRAKRSVRT--- 245
QY 234 DHPTGVWPLHPLF--CALPYH-----SLLLPHLLSAFSGLPALDGSQCGLQDME 281
Db 246 -----IAVLAVFALCFPFHVTTRTYYSFSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPQSPVLSFKGKNNRVLQKLRQNKLGHEHPA-GRKRCPCGLNRS 332
Db 294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSFATPARTLGLRRS 339

RESULT 14
US-08-559-524A-3
; Sequence 3, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-559-524A-3

Query Match      21.1%; Score 382.5; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

QY 15 CQSEKYYQVYLSLAYSIIIFILGLPLNGTVLWHFQGTKRWSCATTYLVNLMVADLLYVL 74
Db 25 CRFNEDFYVLLPVSYGVVGVLCGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQFLGVCHPLCSLPY 133
Db 85 SLPLLVYYARGDHPFSTVLCKLVRFYFNLYCSILFLTCTISVHRCGLGVLRPLRSRW 144
QY 134 RTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSONENFDRLFYAGIVLTL 193
Db 145 GRARYARRVAGAVVVLACQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLGHFGVLF-----TDGQEPDQARGEHPEDRQHSQVHP 233
Db 202 ---LGLL---FAVPAVILVCVLMARLLKPAYGTSG-----GLPRAKRSVRT--- 245
QY 234 DHPTGVWPLHPLF--CALPYH-----SLLLPHLLSAFSGLPALDGSQCGLQDME 281
Db 246 -----IAVLAVFALCFPFHVTTRTYYSFSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPQSPVLSFKGKNNRVLQKLRQNKLGHEHPA-GRKRCPCGLNRS 332
Db 294 SANSC-----LDPVLYFLAGQRLVRFARDAKP-PTGPSFATPARTLGLRRS 339

RESULT 15
US-08-749-707-3
; Sequence 3, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000

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; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-707-3

Query Match      21.1%; Score 382.5; DB 2; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

Qy 15 QFSEKYNQVYLSAYSIIFILGUPLNQTVLWHFWGQTKRWSGATTVLVNLMVADLLYL 74
Db 25 CRFNEDFKYLLPVSYGVVGVCLNAGVLIIFLCRLKTNASTTVMFHLAVSDALYAA 84

Qy 75 -LPELIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLTICISVHQFLGVCHPLCSLPY 133
Db 85 SLPLLVYYARGDHWPFSTVLCVLRFLFYTNLYCSILFLTCISVHRCLGVLRFLRLRW 144

Qy 134 RTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 193
Db 145 GRARYARRVAGAVVVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy 194 SGFLSLIGHFGVLF-----TDGQEPDQARGEPEHEDRQHSQVHP 233
Db 202 ---LGLL--FAVPPAVILVCYVLMARRLLKPAYGTSG-----GLPRAKRSVRT---- 245

Qy 234 DHPTGVWPLHPLF--CALPYH-----SLLLPHLLSAFSGLPALDGSQCGLQDME 281
Db 246 -----IAVLAVFALCFLPFHVTTLTYSPFRSLDLSCHTLNAIN-----MAYKVTRLA 293

Qy 282 ASGCEQQLPQSPVLSFKGKGKRVRLQLKLRQNKLGHPA-GRKRCPCGLNRS 332
Db 294 SANSCL-----LDPVLYIFLAGQRLVRFARDAKP-PTGSPATPARRTLGLRRS 339
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Job time : 47 secs

GenCore version 5.1.7
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12: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.4	18.9	2011	11	US-11-136-527-3805
2	179	17.9	1428	7	US-10-995-561-28
3	179	17.9	1428	7	US-10-995-561-13208
4	166.4	16.6	2693	11	US-11-136-527-3005
5	165.2	16.5	2684	11	US-11-136-527-3527
6	158.4	15.8	1945	11	US-11-136-527-1845
7	147.8	14.8	1400	11	US-11-136-527-5941
8	138	13.8	551	7	US-10-980-388-32
9	107.4	10.7	3122	11	US-11-127-877-9
10	104.2	10.4	3288	11	US-11-136-527-3178
11	99	9.9	1685	7	US-10-750-185-36071
12	99	9.9	1685	7	US-10-750-623-36071
13	94	9.4	1116	11	US-11-134-811-3
14	92	9.2	1428	11	US-11-136-527-3246
15	90	9.0	1423	11	US-11-136-527-2066
16	89	8.9	246360	11	US-11-121-086-8
17	87.6	8.7	1112	11	US-11-134-811-1
18	85.4	8.5	3635	11	US-11-136-527-2101
19	82	8.2	1002	8	US-11-040-218-76
20	82	8.2	1044	8	US-11-040-218-78
21	82	8.2	1095	8	US-11-040-218-80

22	82	8.2	1137	8	US-11-040-218-82	Sequence 82, Appl
23	80.4	8.0	1782	11	US-11-136-527-3486	Sequence 3486, Ap
24	79.6	7.9	1116	11	US-11-136-527-2638	Sequence 2638, Ap
25	79.6	7.9	1116	11	US-11-134-811-5	Sequence 5, Appl
26	78.8	7.9	1102	7	US-10-955-054A-121	Sequence 121, App
27	78.8	7.9	1225	7	US-10-955-054A-112	Sequence 3, Appl
28	78.8	7.9	1662	11	US-11-028-922A-3	Sequence 141, App
29	78.8	7.9	8747	7	US-10-955-054A-141	Sequence 30, Appl
30	77	7.7	1523	11	US-11-127-877-30	Sequence 321, App
31	75.4	7.5	1238	7	US-10-995-561-321	Sequence 320, App
32	75.4	7.5	1498	7	US-10-995-561-320	Sequence 15, Appl
33	75.4	7.5	4267	11	US-11-127-877-15	Sequence 13298, A
34	75.4	7.5	86131	7	US-10-995-561-13298	Sequence 2457, Ap
35	74.4	7.4	1290	11	US-11-136-527-2457	Sequence 6553, Ap
36	74.4	7.4	1290	11	US-11-136-527-6553	Sequence 4, Appl
37	73.6	7.3	1050	11	US-11-028-922A-4	Sequence 2630, Ap
38	73.6	7.3	1651	11	US-11-136-527-2630	Sequence 2159, Ap
39	73	7.3	1384	11	US-11-136-527-2159	Sequence 2954, Ap
40	71.8	7.2	2955	11	US-11-136-527-2954	Sequence 35, Appl
41	69.4	6.9	536	7	US-10-980-388-35	Sequence 2458, Ap
42	69.4	6.9	1163	11	US-11-136-527-2458	Sequence 3673, Ap
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C 45	68.6	6.8	1224	7	US-10-750-623-40492	

ALIGNMENTS

RESULT 1
US-11-136-527-3805
; Sequence 3805, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3805
; LENGTH: 2011
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3805

Query Match	18.9%	Score 189.4	DB 11	Length 2011
Best Local Similarity	53.7%	Pred. No. 2.1e-40		
Matches 461	Conservative 0	Mismatches 391	Indels 7	Gaps 3
QY	43	TGCCAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTT	102	
Db	556	TGTCGCTTCAACGAGGACTTCAAGATATGTGCTGCTGCCCGTCTCTATGGCGTGTGTGC	615	
QY	103	ATCTAGGGTGGCCACTAAATGGCACTGTCTTTGGGCACTTCTGGGGGCAACCAAGCGC	162	
Db	616	GTGCTCGGGCTGTGCTGGAACGTGCTGCCCTCTACATCTTCTGTGGCGCTCAAGACC	675	
QY	163	TGGAGCTGTGCCACCACTATCTGGTGAACCTGATGGTGGCGGACCTCTTTATGTGCTA	222	
Db	676	TGGAACGCTTCCACCCACTACATGTTTCACTGGGAGTTTCTGACTCTCTCTACGACGC	735	
QY	223	T---TGCCCTTCTCTCATCATCACTTCTCACTAGATGACAGGTGGCCCTTCGGGAGCTG	279	
Db	736	TCCCTGCGCTGCTGGTTTATTACTACGCCAGGTGACCACTGGCCATTAGCACAGTG	795	
QY	280	CTCTGCAAGCTGGTGCACTTCTCTGTCTATATCAACCTTTAGGAGCATCTCTGTCTG	339	
Db	796	CTCTGCAAGCTGGTGCGTTTCTCTTCTTCTACACTAACCTCTACTGAGCATCTCTTCTC	855	

Qy	340	ACCTGCATCTCTGFCACCAAGTTCTCTAGTGTGTGCCACCCACATGTGTTCTGCTGCCCTAC	399
Db	856	ACCTGCATCAGCGTGCAACCGGTGCTCGGGGTCTCGCGCCCTCTGCACTCCCTGAGCTGG	915
Qy	400	CGGACCCGCGAGGCATGCTGGCTGGGCACACGACACCACTTGGGCCCTGTGTGTCCTCCAG	459
Db	916	GGCCATGCCCCGCTATGCCCCGAGTGGCTGCGGTTGTGTGGGTGTGTGCTGGCCTGC	975
Qy	460	CTGCTGCCCAACACTGGGCTTCTCCACACGAGCTACATCAATGCGCCAGATGATCTGGTAT	519
Db	976	CAGGCAACCGTGCTCTACTTTGTTCACACACGCGTGAGAGGACCCGAATCACTTGGCCAC	1035
Qy	520	GACATGACAGCCAAAGAAATTTTGATGGCTTTTTCCTACGGCAAGTCTTGACATG	579
Db	1036	GACACTCGGCCCGAGAGCTCTTTAGGCATTTTGTGGCTTACAGCTCTGTCAATG-CTGGG	1094
Qy	580	TCTGGCTTTCTTCCCTCTGGTTCATTTTGGTGTGTATTCACTGATGTGTGAGGACCT	639
Db	1095	TCTGCTTTTGTCTGTGCCCTTTTCCATCATCTCTGCTCTGTTCAGTGCTCATNGGCCGACG	1154
Qy	640	GATCAAGCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCG	699
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Qy	700	GACCATCTGTGTGTGGCTCTTCAACCTCTGTGTTTTGTGGCCTTCCATATCACTCG	759
Db	1215	CACCATCGCCTTAGTACTTGGCCGCTTTTCGCCCTCTGCTTCTGCTTTCACACGTCAACCG	1274
Qy	760	CTCCTTCTACCTCAACCATCTGCTTTCCTTCTCAGGACTGCCAGCTCTTGTATGGCAGC	819
Db	1275	CACCTCTATTACTCTCTTCGATCA---CTTGACCTCAGTTGGCCACACCCTCAACGGCAT	1331
Qy	820	CAGTGTGGCCTTACAAGATATGGAGGCTCTGGTGAGTGTGAGCAGCTGCTCAACCCAGT	879
Db	1332	CAACATGGCGTATAAGATCAACCGGCCACTGGCCAGCGCCAAACAGTTGCTTGCACCTGT	1391
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Db	1392	GCTCTACTTCTGCGAGG	1410

RESULT 2

[illegible]

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	Best Local Similarity	53.8%;	Pred. No. 1e-37;		
	Matches 479;	Conservative 3;	Mismatches 393;	Indels 16;	Gaps 5;
Qy	42	CTGCCAGTTCTCAGAGAAGTCAACGCAAGTCTACCTCTCCCTGGCCTACAGTATCAATCTTT	101		
Db	258	CTGTTGTTTTCATGAGGATTTCAGTTTCATCTGCTGCTGTGAGCTATGCAGTTGTCCTT	317		
Qy	102	TATCCTAGGGCTGCCACTAAATGGCACTGTCCTTGTGGCACTTTCTGGGGCCAAACCAAGCG	161		
Db	318	TGTCCTGGGCTTGGCCCTTAAGCCCAACCCCTATGCTCTTCACTTCGCGCTCCGACC	377		

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RESULT 3
US-10-995-561-13208
; Sequence 13208, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13208
; LENGTH: 13428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13208

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Db	378	CTGGGATGCAACGGCCACCTACATGTTCCACCTGGCATTTGTCAGACACCTTGATGTGCT	437
Qy	222	AT-----TGGCCTTCTCATCATCACTTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCT	278
Db	438	GTGCCTGCCCAACCCCTCATCTACTATTATGAGGCCCAACACACTGGCCCTTTTGGCACTGA	497
Qy	279	GCTCTGCAAGCTGGTGACACTTCCCTGTTTCTATATCAAGCTTTACGGCAGCACTCTGCTGCT	338
Db	498	GATCTGCAAGTGTGTCCGCTTCTTTTCTATATGGAACCTCTACTGTGAGTGTCTTTTCTCT	557
Qy	339	GACCTGCATCTGTGTGACCAAGTTCCTAGGTGTGTGCCACCACTGTGTTGCTGCCCTTA	398
Db	558	CACCTGCATCAGCGTGCACCGCTACCTTGGGCATCTGCCACCCACTTCGGGCACCTACGCTG	617
Qy	399	CCGGACCCGACGGCATCGCTGGCTGGGGCACGAGCACCACTTGGGCCCTTGGTGGTCTTCCA	458
Db	618	GGGCGCGCTCGCTCGCAGGCCCTTCTCGCTGGCAGTTTGGTTGTGTGATGCGCGGTG	677
Qy	459	GCTGCTGCCCACTTGGCCCTTCTCCACACGGACTACATCAATGGCCAGATGATCTGGTA	518
Db	678	CCTCTGCCCAACCTGTCTTTGTCTCAACACGACGACAAAGGACACACGCTCTGTGCCA	737
Qy	519	TGACATGACAGGCCAAGAGAAATTTGATCGCGCTTTTTCCTACGGCANAGTCTTGACATT	578
Db	738	TGACACCACTCGGCYTTGAAGAGTTTGACCACTATGTGCACTTCACTCGGCGGTGATGGG	797
Qy	579	GTCTGGGCTTT--CTTTCCCTCTTGGTCAATTTGGTGTGCTATTCACTGATGGTCAGGAG	636
Db	798	GCTGCTCTTTTGGCGTGCCCTCGCTGGTGCATCTCTGTTTGTATGGACTCATGGCTCGTGC	857
Qy	637	CCTGATCAAGCCAGAGAGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGTCCCAT	696
Db	858	CCTGTATAGCCCTTG-----CCAGGCKTGCACAGTGTCTTCTCGCCTCCGTTCTCT	911
Qy	697	CCGAGCAATCCTACTGGTGTGTGGCTCTTTCAACCCCTGTGTTGTGGCTTTCCATATCAC	756
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Qy	757	TGGCTCTCTTACCTCAACATCTGCTTTCGCTTCTTTCAGGACTGCGACGCTCTTGATGGC	816
Db	972	CCGACCAATTTACTACTCGGCCAGGCTGTTTGGAACT--GACTTGGCGAGTACTGAACAT	1028
Qy	817	AGCCAGTGTGGCCTTACAAGATATGGAGGCCTCTGGTGAGTGTGAGCAGCTGCCCTCAACCC	876
Db	1029	TGTCACGCTGGTCTATAAAGTGACTCGGCCCTGGCCAGTGCCAAAGCTGCTTGGATCC	1088
Qy	877	AGTCTCTACTTTTCTTCAAGGGGGGCAAAATAGATCAGGCTCTCTCCAG	927
Db	1089	TGTGCTCTACTTGC--TCACTGGGGCAAAATATCGAGGTCAAGCTCAGCTCTCTCAG	11137

Query Match 17.9%; Score 179; DB 7; Length 13428;
Best Local Similarity 53.8%; Pred. No. 2.5e-37;
Matches 479; Conservative 3; Mismatches 393; Indels 16; Gaps 5;
42 CTGCAGTTCTCAGAGAGTCAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101
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6257 CTGTTGGTTTGTATGAGGATTTTCAGTTTCATCTCTGCTGCTGAGCTATGCAAGTTGCTT 6316
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102 TATCTAGGCTGCCACTAAATGCACTGTTCTTGGCACTTCTGGGGCCAAACCAAGCG 161
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
6317 TGTCTGGCTTGGCCCTTAACGCCCAACCACTATGCTCTTTCATCTTCCGCTCCGACC 6376
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
162 CTGAGCTGTGCCACCACTATCTGTGGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCT 221
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6377 CTGGATGCAAGCGCACTACATATGTTCCACTGGCATTTGTGACAGACCTTGTATGTCT 6436
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
222 AT---TGCCTTCTCATATCATCACTACTCACTAGATGACAGTGGCCCTTTCGGGAGCT 278
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6437 GTGCTGCCACCTCATCTACTATTATGACAGCCCAACCACTGGCCCTTTTGGCACTGA 6496
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
279 GCTCTGCAAGTGTGACTCTCTCTGTTCTATATCAACCTTTACGGGACATCTCTGCTGCT 338
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
6497 GATCTGAAGTTCCTGCGCTTCTTCTATTGGAACCTCTACTGCAAGTGTCTCTTTTCT 6556
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339 GACCTGCATCTCTGTGACCAAGTTCTCTAGGTGTGTGCCACCACTGTGTTGCTGCCCTA 398
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6557 CACTGTGATAGGTGACCGCTACCTAGGTGATCTGCCACCACTTCGGGCACTACGCTG 6616
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6617 GGGCGGCTCGCTCGAGGCTTCTCTGCTGGCAGTTTGGTTGTTGCTAGCGGCTG 6676
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519 TGACATGACCAAGCAAGAAATTTGATCGGCTTTTGGCTACCGCATAGTTCTGACATT 578
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6737 TGACACCACTCGGCTGGAAGATTGTGACCACTATGTGCACTTCAGCTCGGCGGTATGGG 6796
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579 GTCTGGCTTT---CTTTCCTCTTGGTCAATTTTGGTGTGCTTATTCACATGATGTCAGGAG 636
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
6797 GCTGCTCTTTGGCGTGGCTGCTGGTCACTCTTGTGTTGCTATGGACTCATGGCTCGTCG 6856
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
637 CTGATCAAGCCAGAGAACTCATGAGAGCAAGGCAACACAGCCGAGCCAGGTCAT 696
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
6857 CCTGTATCAGCCCTTG-----CCAGGCKCTGCACAGTCTTCTCGCCCTCCGCTCTCT 6910
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697 CCGGACCATCTACTGTGTGTGGCTCTTACCCCTGTTGTTGTCGCTTCCATATCAC 756
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
6911 CCGCACCTAGCTGTGTGTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6970
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
757 TCGCTCTCTTACCTCAACATCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGTATGGC 816
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
6971 CCGCACCATTTACTCTGGCCAGGCTGTGGAAGCT---GACTGCGGAGTACTGAACAT 7027
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
817 AGCCAGTGTGCCCTACAGATATGAGGCTCTCTGAGTGTGAGAGTGCCTTCAACCC 876
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
7028 TGTCAAGTGTCTATAAAGTGACTCGGCCCTGGCCAGTGCCAAGAGTCTGCTGGATCC 7087
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
877 AGTCTGTACTTCTTCAAGGGGGGCAAAATATAGATCAGGCTCTCTCCAG 927
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
7088 TGTGCTCTACTTGC---TCACCTGGGGCAAAATATCGACGTACGCTCCRTFCAG 7136

RESULT 4
US-11-136-527-3005
; Sequence 3005, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3005
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3005

Query Match 16.6%; Score 166.4; DB 11; Length 2693;
Best Local Similarity 53.5%; Pred. No. 2.9e-34;
Matches 483; Conservative 1; Mismatches 402; Indels 16; Gaps 6;
31 GAACAAGTCTCTGCCAGTTCTCAGAGAAGTACAGAAGTCTACCTCTCCCTGGCCTAC 90
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1421 GGAGATGGTGTAGTTTAAATGAGAGTTCAAGTTTCATCTCTGTTGCCCTATGAGCTAT 1480
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
91 AGTATCATCTTTATCCCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGC 150
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1481 GCAGTTGTGTTGTGCTGGGCTGGCCCTCAATGCTCAACCTCTGGCTGTCTCTCTTC 1540
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 CAAACCAAGCGCTGGAGCTGTGCCACCACTATCTGTGAACCTGTATGTTGGCGGACCTG 210
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1541 CGCCTTCGACCTCGGGATGCAACAGCACCTACATGTTCCACCTGGCATTTGTTCAGACAC 1600
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
211 CTTTATGTGCTAT---TGCCTCTCTCATCATCACTACTACTAGATGACAGTGGGCC 267
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1601 TTGTAATGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1660
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
268 TTCGGGAGTGTCTGCAAGCTGGTGCACTTCTGTTTATATCAACCTTTACGGGAGC 327
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1661 TTTGGCACTGGCCCTTTCGAAAGTTTGTCCGCTTCTCTCTTATTGGAACCTCTACTAGT 1720
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
328 ATCTGTGTGCTGACCTGCTGTCACCACTCTGTCAGCAGTTCCTAGGTGTGCCACCACTGT 387
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1721 GTCTTTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1780
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
388 TCGTGTCTTACCGGACCCGCGAGCATGCTGGCTGGGACCAAGCACCACCTGCGGCCCTG 447
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1781 GCAATCGCTGGGGCGCCCTCGATTTTGCAAGCTTCTCTGCTGCTGGGTGTTGTTGGTA 1840
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
448 GTGTCTCTCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1841 GTAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1900
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
508 ATGATCTGTTATGACATGACCCAGAGAAATTTTTCATCGGCTTTTTCCTACGGCATA 567
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1901 ATCTGTGCTATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1960
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
568 GTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 625
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1961 GCAGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2020
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
626 ATGCTCAGGAGCTGATCAAGCCAGAGAGAACTCATGAGGACAGGCAACACAGCCGGA 685
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2021 ATGGCCCGGAGCTGTATCGACCTTTG---CCAGGAGCTGACAGCTCA---TCTTCTCGG 2074
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
686 GCCAGGTTCATCCGGACCATCTACTGTTGTGGGCTCTTACCCTCTGTTTGTGTCGCC 745
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2075 CTCGGTTCCCTCCG7ACCATTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2134
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
746 TTCCATATCACTGCTCTTCTTACCTCACTCTGCTTCTGCTTCTGCTTCTCAGGACTGCCAG 805
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2135 TTCCATATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2191
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
806 CTCTTGTAGGAGCAGTGTGGCTTACAGATATGAGGCTCTGTTGAGTGTGAGGAGC 865
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2192 GTGCTGAACATTTGCAATGTTGTTTCAAGGTGACTCGACCCCTGGCAGTGTCTAATAGC 2251

QY 866 TGCTCAACAGCTCTGTACTTCTTTCAAGGGGCAAAAATAGAGTCAGGCTCTCC 925
DB 2252 TGTCTGATCCAGTCTCTA--TCTCTTCAAGGGGCAAAAGTATCGAAACAGCTCCAGC 2309
QY 926 AG 927
DB 2310 AG 2311
RESULT 5
US-11-136-527-3527
; Sequence 3527, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3527
; LENGTH: 2684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3527

Query Match 16.5%; Score 165.2; DB 11; Length 2684;
Best Local Similarity 53.5%; Pred. No. 6.1e-34;
Matches 483; Conservative 0; Mismatches 403; Indels 16; Gaps 6;
QY 31 GAACAAGTCTCTGCCAGTCTCTCAGAGAAGTACAAAGTCTACCTCTCCCTGGCCTAC 90
DB 1412 GGAGATGGTATTTAGTATTAATGAGAGTTCAAGTTCACTCTGTTGCCATGAGTAT 1471
QY 91 AGTATCATCTTTAFCCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGC 150
DB 1472 GCAGTTGTGTTGGCTGGGCTGGCCCTCAATGCTCAACCCCTCTGGCTTCTCTTC 1531
QY 151 CAACCAAGCGCTGGAGCTGTGCCACCACTATCTGTGTAACCTGATGGTGGCGAGCTG 210
DB 1532 CGCCTTCGACCTGGGATGCAACAGCCACCTACATGTTCCACCTGGCATTTGTCCAGACC 1591
QY 211 CTTTATGTGTAT--TGCCCTTCTCATCATCACTACTCTACTAGATGACAGTGGCCC 267
DB 1592 TTGTATGTGTGTCACTGCCCCACCCTCGTCTACTATGCTGCGAGAAACCACTGGCCC 1651
QY 268 TTCGGGAGCTGTCTCTCAAGCTGGTGCACTTCTCTGTATATATCAACCTTTACGGCAGC 327
DB 1652 TTTGGCACTGGCCTTTGCAAGTTGTTCGGCTTTCTCTTCTATTTGGAACCTCTACTGTAGT 1711
QY 328 ATCTGCTGTGACTGTGATCTGTGTCACAGTTCCTTAGTGTTGTCACCACTGTGT 387
DB 1712 GTCTTTTCTCTCACTGCATCAGTGTGCACGATACCTGGGTATCTGCCACCACTCGG 1771
QY 388 TCGTGTCCCTACCGAGCCCGAGCATGCTGGCTGGGACCCAGCACCACTGGCCCTG 447
DB 1772 GCAATCGCTGGGGCCGCCCTCGATTTGCAAGCTTCTCTGCTGGGTGTTGGTAT 1831
QY 448 GTGTCTCTCAGCTGTCTGCCACACTGGCCCTTCTCCACAGGCACTACATCAATGGCCAG 507
DB 1832 GTAGCTGCTGCTCGTGGCCCAATCTTTCTTTGTGACAACTCAATGCAACTACC 1891
QY 508 ATGATCTGGTATGATGATGACAGCAAGCAAGATTTTGTATGGCTTTTGTGCTACGGGATA 567
DB 1892 ATCTGTGCCATGACACTACTCTGCCAGAGAGTTTGACCACTACGCTACTCTCAGTTCG 1951
QY 568 GTTCTGACATTTCTGCTGCTT--CTTTCCCTCTGTGCTATTTTGGGTGCTATTCACTG 625

DB 1952 GCAGTCATGTGTGCTCTTTGGTTGGCCCTTCTTGTATCACCCTGGTCTGCTATGGACTC 2011
QY 626 ATGGTCAGGAGCTGTATCAAGCCAGGAGAACTTATGAGGACAGGCAACACAGCCCGA 685
DB 2012 ATGGCCCGGCGAGCTGTATCGACCTTTG---CCAGGAGCTGGACAGTCA--TCTTCTCGG 2065
QY 686 GCCAGGTCCATCGGACCACTCTACTGGTGTGTGGCTCTTCAACCCTCTGTTTGTGGCCC 745
DB 2066 CTCGGTTCCCTCGTACCATTTGCTGTGGNGCTGACTGTCTTTGCTGTCTCTCGTGCCT 2125
QY 746 TTCCATATCACTCGCTCTCTTCTACTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAG 805
DB 2126 TTCCACATCACCCGCACAATTTATTACCAGGCAAGACTGTTGCAAGCT---GACTGTCTAT 2182
QY 806 CTCTTGTATGGCAGCAGTGTGGCTCAAGATATGAGAGGCTCTGTGTGATGTGAGCAGC 865
DB 2183 GTCTGAACATTTGCAATGTGTTTACAAGGTGACTCGACCCCTGGCCAGTGTCTAATAGC 2242
QY 866 TGCTCAACCCAGTCTGTACTTTCTTCAAGGGGGCAAAAATAGAGTCAGGCTCTCTCC 925
DB 2243 TGTCTTGATCCAGTGTCTTA--TCTCTTCAAGGGGGCAAAAGTATCGAAACAGCTCCAGC 2300
QY 926 AG 927
DB 2301 AG 2302

RESULT 6

US-11-136-527-1845
; Sequence 1845, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1845
; LENGTH: 1945
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-1845

Query Match 15.8%; Score 158.4; DB 11; Length 1945;
Best Local Similarity 51.2%; Pred. No. 3.4e-32;
Matches 437; Conservative 4; Mismatches 405; Indels 8; Gaps 3;
QY 42 CTGCGAGTCTCAGAGAAGTACAAAGTCTACCTCTCCCTGGCCTTACAGTATCATCTT 101
DB 490 CTGCGTCTACGTGAGGATTTCAAGCGACTGTCTGTCTACCCCGAGTTTACTCAGTGTGCT 549
QY 102 TATCTTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
DB 550 GGTGTGCGGCTGCCACTGAACGTCGTGTATCGCCAGATATGCGCATCCGCCGCGAC 609
QY 162 CTGAGCTGTGCCACCACTATCTGTGTAACCTGATGGTGGCGGACCTGCTTTATGTGCT 221
DB 610 CTTGACCCGTTCCGCTGTGTACACCTGAACTTTGGCACTGGCGACCTGCTGTATGCTG 669
QY 222 AT---TGCCCTTCTCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTTCCGGGAGCT 278
DB 670 TTTCACTGCCCTTACTTATCTTAATACGCGAGGGGACCACTGGCCCTTTCCGAGACCT 729
QY 279 GCTCTGCAAGCTGGTGCACTTCTCTGTTCTATATCAACCTTTTACGCAAGATCTCTGTGCT 338
DB 730 TGCCTGCGGCTGGTACGCTTCTCTTATATGCAACCTTACACGGCAGCATCTCTGTTCCT 789
QY 339 GACCTGCATCTCTGTGACCACTTCTTAGGTGTGTGCCACCACCTGCTGTTCGCTGCCCTA 398


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; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-980-388-32
;
Query Match      13.8%; Score 138; DB 7; Length 551;
Best Local Similarity 100.0%; Pred. No. 5.3e-27;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGAGTGGACATGATATACATCACAGAAACAAGGCTCTGCGCAGTTCTCAGAGAAG 60
Db 138 ATGAGAGAGTGGACATGATATACATCACAGAAACAAGGCTCTGCGCAGTTCTCAGAGAAG 79

Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTATCCTAGGCTGCCACTA 120
Db 78 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTATCCTAGGCTGCCACTA 19

Qy 121 AATGGCACTGCTGTGTGG 138
Db 18 AATGGCACTGCTGTGTGG 1

RESULT 9
US-11-127-877-9
; Sequence 9, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merck, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 3122
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-9

Query Match      10.7%; Score 107.4; DB 11; Length 3122;
Best Local Similarity 52.3%; Pred. No. 1.4e-18;
Matches 311; Conservative 0; Mismatches 276; Indels 8; Gaps 3;

Qy 72 CTACCTCTCCCTGCGCTACAGTATCATCTTTATCCTAGGCTGCCACTAAATGGCACTGT 131
Db 992 CTACCTGCGGCTGTCTACATCTTTGGTATTATCATCGGCTTCTGGGCAACAGCGTGGC 1051
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Qy 132 CTTGTGGCACTTCTGGGGCCAAACAGCGCTGGAGCTGTGCCACACCTATCTGGTGAA 191
Db 1052 CATCTGGATGTTCTGTCTTCCACATGAAGCCCTGGAGCGGCATCTCCGTGTACATGTTCAA 1111

Qy 192 CCTGATGGTGGCGACCTGCTTTATGTGCTAT---TGCCCTTCTCTATCATCATCACTACTC 248
Db 1112 TTTGGCTCTGGCGACATCTTTGTACGTGCTGATCTTGCGAGCCCTGATCTTCTACTACTT 1171

Qy 249 ACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGGTGACATCTCTGTTCTA 308
Db 1172 CAATAAAACAGATGGATCTTCGGGATGCCATGTGTAAACTGCAGAGGTTTCATCTTTCA 1231

Qy 309 TATCAACCTTTACGGCAGCATCTGCTGCTGACCTGATCTCTGTGCACCAAGTTCCTAGG 368
Db 1232 TGTGAACCTCTATGGCAGCATCTTGTCTTGACATGATCATCAGTGCCTCCACCGGTACAGCG 1291

Qy 369 TGTGTGCCACCCACTGTGTTGCTGCCCTACCGGACCCGAGGCATGCTTGGCTGGGCGAC 428
Db 1292 TGTGGTGTACCCCTCAAGTCCCTGGCGCGCTCAAAAAGAAATGCGATCTGTATCAG 1351

Qy 429 CAGCACCACTGGGCGCTGGTGTCTTCAGCTGTGCTGCCACACACTGGCCCTTCTCCACAC 488
Db 1352 CGTGTGCTGTGGCTCATTTGTGCTGGCGCATCTCCCCCATCTCTTCTACTCAGGTAC 1411

Qy 489 ---GGACTACATCAATGCCAGATGATCTGGTATGATCATGACACCAAGCAAGATTTTGA 545
Db 1412 CGGGGTCCGCAAAACAAACCATCACCTGTTACGACACCACTCAGACGAGTACCTGGC 1471

Qy 546 TCGGCTTTTTCCTAGGCACTGTTCTGACATTTGTC--TGGCTTTTCTTCCCTCCTTGGT 603
Db 1472 AAGTTATTTCATCTACAGCATGTGCAGACCGTGGCATGTTCTGTGCTCCCTTGGTGT 1531

Qy 604 CATTTGGTGTGTATTTACTGATGTGTCAGAGCCTGATCAAGCCAGAGAGAGAAC 658
Db 1532 GATTCTGGGCTGTACGGATTAATTGTGAGAGCTTTGATTTTACAAAGATCTGGAC 1586

RESULT 10
US-11-136-527-3178
; Sequence 3178, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Monte, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3178
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-3178

Query Match      10.4%; Score 104.2; DB 11; Length 3288;
Best Local Similarity 51.9%; Pred. No. 9.8e-18;
Matches 309; Conservative 0; Mismatches 278; Indels 8; Gaps 3;

Qy 72 CTACCTCTCCCTGCGCTACAGTATCATCTTTATCCTAGGCTGCCACTAAATGGCACTGT 131
Db 775 CTACCTGCGCTGCGCTCTACATCTTAGTGTTCATCATAGGCTTCTTGGCAACAGCGTGGC 834

Qy 132 CTTGTGCACTTCTGGGGCCAAACAGCGCTGGAGCTGTGCCACCACTATCTGGTGAA 191
Db 835 AATCTGGATGTTGTGTTTTCACATGAAGCCTTGAGCGGCATCTCGGTGTACATGTTCAA 894

Qy 192 CCTGATGGTGGCGACCTGCTTTATGTGCTAT---TGCCCTTCTCTATCATCACTACTC 248
Db 895 TTTGGCTCTGCGGACCTTTTGTGTGTGCTCACCTACCAGCTCTCATCTTCTACTACTT 954
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Qy	249	ACTAGATGACAGGTTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGGTGACATTTCCTGTTCTA	308
Db	955	CAACAAGACTGACTGGATCTTCGGGGATGTTATGTGAAGCTGCAGAGGTTTCATCTTCCA	1014
Qy	309	TATCAACCTTTTACGGCAGCATCTCTGCTGTGACCTGTGATCTCTGTGCACAGTTTCCTAGG	368
Db	1015	TGTAACCTCTATGGCAGCATCTTTGTTCTCACCTGTCATCAGTGCACACACAGGTACAGTGG	1074
Qy	369	TGTGTGCCACCCACTGTGTTCGTGCCCTACCCGACCCGAGGACATGCCCTGGCTGGGCAC	428
Db	1075	CGTGGTGTACCCCTCTCAAGTCTCTGGGCGAGCTCAGAAGAAGAAATGCCATTTATGTGCAG	1134
Qy	429	CAGCACCACTGGGCCCTGGTGGTGCTCCAGCTGCTGCCACACTGGCTTCTCCCCACAC	488
Db	1135	TGTGCTGGTATGGCTCAATTGTGGTGGTGCCCATCTCCCCCATCTCTTCTACTCTGGCAC	1194
Qy	489	GGACTACATCAATGGCCAGA---TGATCTGGTATGACATGACACAGCCAAAGAGATTTTGA	545
Db	1195	TGGGATTCGGAAAAACAACATGTCACCTGCTACGACTCCACGTCAGATGAGTACCTGCG	1254
Qy	546	TCGGCTTTTGGCCTAAGGCATAGTPTCTGACATGTC--TGCGTTTCTTTTCCCTCCTTTGGT	603
Db	1255	AAGTTATTTTCATCTACAGTATGTGCACGACTGTGGCCATGTTCTGTCATCCGCCCTGGTGCT	1314
Qy	604	CATTTTGGTGTCTATTCACTGATGGTGCAGAGCCTGATCAAGCCAGAGAGAAC	658
Db	1315	GATCTTGGGTGTATGGATTAATTTGTTAGAGCTTTGATCTACAAAGATCTGCAG	1369

RESULT 11

```

US-10-750-185-36071/c
; Publication 36071, Application US/10750185
; Sequence No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFE
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-36071

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Query Match	9.9%	Score 99	DB 7	Length 1685
Best Local Similarity	50.7%	Pred. No. 1.8e-16		
Matches 237	Conservative 0	Mismatches 230	Indels 0	Gaps 0
Qy	71	TCACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTAAATGGCACTG	130	
Db				
	1337	TCCTCATCTCTTTTCATCTATCCCTGGTGTGCTCTGTGGGCTCTGTGGNACTCCATGG	1278	
Qy	131	TCCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACCTATCTGGTGA	190	
Db	1277	TCATCTACGTGATCCTCGGCTACGCCAAGATGAAGAGCGGCCACCAACATCTACATCTCTCA	1218	
Qy	191	ACCTGATGGGGCGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATCACCTACTACAC	250	
Db	1217	ACCTGGGCATCGCGATGAGCTGCTATGCTCAGCGTGCCCTCTCTGGTCACTCCACAT	1158	
Qy	251	TAGATGACAGGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATCTCTCTGTTCTATA	310	

RESULT 12

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US-10-750-623-36071/c
; Sequence 36071, Application US/10750623
; Publication NO. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10750, 623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-623-36071

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Query Match	9.9%	Score 99	DB 7	Length 1685
Best Local Similarity	50.7%	Pred. No. 1.8e-16		
Matches 237	Conservative 0	Mismatches 230	Indels 0	Gaps 0
Qy	71	TCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGCTGCCACTAAATGGCACTG	130	
Db	1337	TCCTCATCTCTTTTCATCTACTCCGTGTGTCTGTGGGGCTCTGTGGAACTCCATGG	1278	
Qy	131	TCCTTGTGGCACTTCTGGGGCAAAACCAAGCGCTGGAGCTGTGCCACCACCATCTCTGGTGA	190	
Db	1277	TCATCTACGTGATCTCTGGCTAGCCCAAGATGAAGCGGCCACCAACATCTACATCTCTCA	1218	
Qy	191	ACCTGATGTGTGGCGGACCTGCTTTATGTGTATTTGCCCTTCTCTCATCATCACCTACTCAC	250	
Db	1217	ACCTGGCCATCGCGCGATGAGCTGCTATGCTACAGCGTGCCCTTCTCTGGTCACTTCCACAT	1158	
Qy	251	TAGATGACAGGTGGCCCTTCGGGGAGTGCTCTGCAGCTGGTGCACTTCTCTGTTCTATA	310	
Db	1157	TGCTTGCACCATGCCCCCTTCGGCGCGCTACTCTCGCGCCTCTGCTCAGCGTGACGCCAG	1098	
Qy	311	TCAACCTTTTACGGCAGCATCCTGTGTGTGACCTTGCATCTCTGTGCACCAGTTCCTTAGGTG	370	
Db	1097	TCAACATGTTTACCAGCATCTACTGTCTGACTGTGCTTAGCGTGGACCGCTACGTGSCCG	1038	
Qy	371	TGTGGCAACCCATGTGTGTCTGCCCTTACCGGACCCGACGAGCATGCTGTGCTGGGACCA	430	
Db	1037	TGTGTGCAACCCCATCAAGCGCGCACGCTTACCGCGCGGCCACCGTGGCCAAAGTGTGTGAATC	978	

Qy 431 GCACACCTGGCCCTGGTGTCTCCAGCTGCTGCCACACAGTGGCTTCTCCACACGG 490
Db 977 TGGCGTGTGGTGTCTGGTGTCTCCAGCTGCTGCCACACAGTGGCTTCTCCACACGG 918
Qy 491 ACTACATCAATGGCCAGATGATCTGGTATGATGACATGACACGACAGAG 537
Db 917 CGGCCAACAGCAGCGGACCGTGGCTGCCAACATGCTCATGCCCGAG 871

RESULT 13
US-11-134-811-3
; Sequence 3, Application US/11134811
; Publication No. US20060024750A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2043
; CURRENT APPLICATION NUMBER: US/11/134,811
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: PCT/EP02/07647
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-134-811-3 ;

Query Match 9.4%; Score 94; DB 11; Length 1116;
Best Local Similarity 50.2%; Pred. No. 3.2e-15;
Matches 232; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

Qy 70 GTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTAAATGGCACT 129
Db 115 GTCTTCTGTGGTGTATCTACAGCTTGGTGTCTCTCGTCTCCCTAGGCAACGGCTG 174
Qy 130 GTCTTGTGGCACTTCTGGGGCAACCAACGCGCTGGAGCTGTGCCACCACTAFTCTGGTG 189
Db 175 GTGATGTCATCGCCACCTTCAAGATGAAGAAGACCGTGAACACTGTGTGTTGTCAAC 234
Qy 190 AACTGATGTGGCGGACCTGCTTTATGTGCTATTGGCTTCTCCATCATCACTACTCA 249
Db 235 CTGGCTGTGGCGGACTTCTCTTCAACATCTTTTGGCGATGCACTCACCTACGCGGCC 294
Qy 250 CTAGATGACAGTGGCCCTTCGGGGAGCTGCTCGCAAGCTGGTGCACTTCTCTTCTAT 309
Db 295 ATGACTTACCACTGGGTGTTCCGGAAGGCCATGTGAAGATCAGCAACTTCTTCTCAGC 354
Qy 310 ATCAACCTTTACGGCAGCATCTCTGCTGACCTGCACTCTCTGTGCCACCACTTCTAGGT 369
Db 355 CACAACATGTACACCGGCTTCTCTGCTGACTGTCACTAGCTTTGACCGCTGCACTCC 414
Qy 370 GTGTGCCACCACTGTGTGCTGCTGCCCTACCGGACCGGAGCATGCTGTGGGCAAC 429
Db 415 GTGTGCTCCCGCTGTGTGCTCCAGAACCGCAGCATCGGCTGGGCTACATGACCTGC 474
Qy 430 AGCACCACTGGGCGCTGTGGTCTCTCCAGCTGCTGCCACACCTGGCTTCTCCACACG 489
Db 475 TCGGCGCTGTGGGTCTTCTTCTTGTAGCTCCCGGTCCTTGTCTTCCGGGACAC 534

Qy 490 GACTACATCAATGCCAGATGATCTGGTATGACATGACACGAGC 531
Db 535 GCCAACATTTCATGGGAAGATAAAGCTGCTTCAACAACTTCAGC 576

RESULT 14
US-11-136-527-3246
; Sequence 3246, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3246
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3246

Query Match 9.2%; Score 92; DB 11; Length 1428;
Best Local Similarity 56.5%; Pred. No. 1.2e-14;
Matches 192; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

Qy 50 TCTCAGAGAAGTCAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAG 109
Db 206 TCACCGGGAAGCTGACCCAGCTCTTTCTCCCGGTCACTACATCATCTTTTGAATTG 265
Qy 110 GGCTGCCACTAAATGGCACTGTCTGTGGCACTTCTGGGCGCAACCAAGCGCTGGAGCT 169
Db 266 GTTGTCCCAAGTAATGGTATGGCCCTCTGGGTCTTTCTTCCGAACGAAGAAGCACC 325
Qy 170 GTGCCACCACTATCTGGTGAACCTGATGTGGCGGCACTGCTTTATGTGCTATTTGCCCT 229
Db 326 CTGCTGTGATTACATGGCCAACTGGCCTTGGCAGACCTCTCTGTCTATCTGGTTCC 385
Qy 230 TCTCATCATCACTACTACTCATAGATG---ACAGGTGGCCCTTCGGGAGAGCTGCTCTGCA 286
Db 386 CCCTGAAGATCTCTACCACCTCCATGGCAACGACTGGACCTATGGGGATGCGCTCTGCA 445
Qy 287 AGCTGGTGCACTTCCCTGTTCTATATCAACCTTTTACGCGCAGCATCCTGCTGTGACCTGCA 346
Db 446 AGGTGCTCATTTGGCTTTTCTCGGCAATATGACTCTCATCTCTTTTCATGACCTGCC 505
Qy 347 TCTCTGTGACCACTTCTTAGGTGTGTGCCACCCCACTGTG 386
Db 506 TCAGCGTGACAGAGTACTGGGTGATCGTGAACCCCATGGG 545

RESULT 15
US-11-136-527-2066
; Sequence 2066, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2066
; LENGTH: 1423


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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2066 ;

Query Match      9.0%; Score 90; DB 11; Length 1423;
Best Local Similarity 52.4%; Pred. No. 4.1e-14;
Matches 198; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 71 TCTACCTCTCCCTGGCTACAGTATCATCTTATCCTAGGGCTGCCACTAAATGGCACTG 130
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 254 TCGCCATACGCGCCTCTACTCGGCTGTGTGCGCCGTGGGGCTGTGGGCAACGTGCTCG 313
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 131 TCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACCTATCTGGTGA 190
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 314 TCATGTTGGNAATCGTCGGGTACACTAAGCTGAAGACGGCCACCACATCTACATCTTCA 373
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 191 ACCTGATGGTGGCCGACCTGCTTTATGTGTATTTGCCCTTCTCATCATCACCTACTCAC 250
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 374 ATCTGGCCTTGGCGGATGCGCTGGCCACCAGCACACTGCCCTTCCAGAGCGCCAAGTACC 433
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 251 TAGATGACAGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGGTGCATTCCTGTTCTATA 310
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 434 TGATGGAACGCTGGCCGTTGGAGAGCTGTGTGCAAGGCTGTGCTCTCCATTGACTACT 493
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 311 TCAACCTTTACGGCAGCATCCTGCTGTGACCTGCATCTCTGTGCACAGTTCCTAGGTG 370
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 494 ACAACATGTTACACAGCATCTTCACGCTCACCATGATGAGCGTGGACCGCTACATTGGGG 553
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 371 TGTGCCACCCACTGTGTGCTGCCCTACCGGACCCCGCAGGCATGCTGTGGCTGGGCACCA 430
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 554 TCTGCCACCCCTGTCAAGGCTTGGACTTCCGGACACCGGCCAAGGCAAGCTGATCAACA 613
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 431 GCACCACCTGGGCCCTGG 448
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 614 TATGCATCTGGGCTTGG 631
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: February 15, 2006, 11:45:42

Job time : 295 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 11:15:22 ; Search time 992 Seconds
(without alignments)

8352.739 Million cell updates/sec

Title: US-10-088-726-25

Perfect score: 1002

Sequence: 1 atggagaaggaggacatgaa.....ggttgaaacagatctgggtaa 1002

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1002	100.0	1002	6	US-10-088-726-25
2	1000.4	99.8	1334	6	US-10-017-161-707
3	1000.4	99.8	1334	6	US-10-292-798-619
4	1000.4	99.8	3143	6	US-10-275-910-1
5	996.4	99.4	1082	6	US-10-023-586B-1
6	996.4	99.4	1082	7	US-10-763-972-1
7	977.4	97.5	1108	7	US-10-072-012-165
8	920.4	91.9	1017	3	US-09-885-453-3
9	920.4	91.9	1017	5	US-10-079-384-5
10	917.2	91.5	1020	6	US-10-023-586B-3
11	917.2	91.5	1020	7	US-10-763-972-3
12	917.2	91.5	1076	7	US-10-333-946-20
13	849.4	84.8	851	6	US-10-275-910-6
14	848.4	84.7	850	6	US-10-275-910-4
15	588	58.7	600	10	US-11-060-756-1747
16	588	58.7	600	10	US-11-060-756-1748
17	588	58.7	600	10	US-11-060-756-6019
18	588	58.7	600	10	US-11-060-756-6020
19	510	50.9	510	3	US-09-782-974C-13
20	510	50.9	510	9	US-10-467-492A-13
21	510	50.9	510	9	US-10-975-979-13
22	510	50.9	510	9	US-10-969-727-13
23	400.4	40.0	681	3	US-09-801-944B-47

24	374	37.3	585	3	US-09-801-944B-56	Sequence 56, Appl
25	229.4	22.9	2025	5	US-10-225-567A-216	Sequence 216, App
26	229.4	22.9	2025	6	US-10-101-510-722	Sequence 722, App
27	229.4	22.9	2025	6	US-10-305-720-1482	Sequence 1482, Ap
28	229.4	22.9	2025	7	US-10-776-827-74	Sequence 74, Appl
29	229.4	22.9	2025	9	US-10-756-149-3861	Sequence 3861, Ap
30	227.8	22.7	2118	6	US-10-101-510-431	Sequence 431, App
31	180.2	18.0	1098	5	US-10-225-567A-331	Sequence 331, App
32	180.2	18.0	1429	3	US-09-077-173A-1	Sequence 1, Appli
33	180.2	18.0	1429	6	US-10-305-720-1068	Sequence 1068, Ap
34	180.2	18.0	1429	8	US-10-753-695-1	Sequence 1, Appli
35	180.2	18.0	1429	8	US-10-811-198-1	Sequence 1, Appli
36	180.2	18.0	1429	8	US-10-811-192-1	Sequence 1, Appli
37	175.4	17.5	1651	6	US-10-366-288-41	Sequence 41, Appl
38	170	17.0	234	3	US-09-801-944B-55	Sequence 55, Appl
39	166.4	16.6	984	6	US-10-278-087A-57	Sequence 57, Appl
40	164.8	16.4	1571	6	US-10-354-358-9	Sequence 9, Appli
41	164.8	16.4	1571	6	US-10-305-720-1108	Sequence 1108, Ap
42	164.8	16.4	1571	9	US-10-756-149-3796	Sequence 3796, Ap
43	164.8	16.4	1832	5	US-10-225-567A-222	Sequence 222, App
44	164.8	16.4	1832	6	US-10-172-118-994	Sequence 994, App
45	164.8	16.4	1832	6	US-10-295-027-1071	Sequence 1071, Ap

ALIGNMENTS

RESULT 1

US-10-088-726-25

; Sequence 25, Application US/10088726

; Publication No. US20030157558A1

; GENERAL INFORMATION:

; APPLICANT: Matsumoto et al.

; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS A

; FILE REFERENCE: 62514

; CURRENT APPLICATION NUMBER: US/10/088,726

; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: PCT/JP00/09408

; PRIOR FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: JP 1999-375152

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: JP 2000-101339

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 1002

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-088-726-25

Query Match 100.0%; Score 1002; DB 6; Length 1002;

Best Local Similarity 100.0%; Pred. No. 2.6e-303;

Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGGAAGAGTGGACATGATACATCAGAAAGGTCTCTGCCAGTCTTCAGAGAAG	60
Db	1	ATGGAAGAGTGGACATGATACATCAGAAAGGTCTCTGCCAGTCTTCAGAGAAG	60
Qy	61	TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA	120
Db	61	TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA	120
Qy	121	AATGGCACTGCTTGTGGCACTTCCTGGGGCCAAACCAAGCGTGGAGTGTGCCACACC	180
Db	121	AATGGCACTGCTTGTGGCACTTCCTGGGGCCAAACCAAGCGTGGAGTGTGCCACACC	180
Qy	181	TATCTGGTGAACCTGATGGCGACCTGCTTTATGTGCTATTGCCCTTCTCTCATCATC	240
Db	181	TATCTGGTGAACCTGATGGCGACCTGCTTTATGTGCTATTGCCCTTCTCTCATCATC	240
Qy	241	ACCTACTCACTAGATGACAGGTGGCCCTTCCTGGGGAGTGTCTCTGCAAGCTGTGCACTTC	300

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Db 241 ACCTACTCCTAGATGAGGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 360
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTGTGCACAG 360
Qy 361 TTCTAGGTGTGCCACCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 TTCTAGGTGTGCCACCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 CTGGGACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 CTGGGACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGGTATGACATGACACGAGCAAGAAAT 540
Db 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGGTATGACATGACACGAGCAAGAAAT 540
Qy 541 TTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 GGTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Qy 721 CCTCTTCAACCTCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 721 CCTCTTCAACCTCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Qy 781 CTTTCTGCTTCTCAGACCTGCCAGCTCTGATGGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 CTTTCTGCTTCTCAGACCTGCCAGCTCTGATGGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 GAGGCTCTGCTGAGTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GAGGCTCTGCTGAGTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 GGCAAAATAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db 901 GGCAAAATAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 GCTGGGAGGAGAGATGCCAGGCTTCAACAGATCTGGGTAA 1002
Db 961 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1002
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RESULT 2
US-10-017-161-707
; Sequence 707, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: SUWA, MAKIYO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 707
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1334)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(715)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(1134)
US-10-017-161-707

Query Match 99.8%; Score 1000.4; DB 6; Length 1334;
Best Local Similarity 99.8%; Pred. No. 9.2e-303;
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAAGAAGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAATGTTCTCAGAGAAG 60
Db 201 ATGGAAGAAGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAATGTTCTCAGAGAAG 260
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 261 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 320
Qy 121 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 180
Db 321 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 380
Qy 181 TATCTGTGAACCTGATGGTGGCGGACCTGCTTTTATGTGCTATTGGCCCTTCTCATCATC 240
Db 381 TATCTGTGAACCTGATGGTGGCGGACCTGCTTTTATGTGCTATTGGCCCTTCTCATCATC 440
Qy 241 ACCTACTCCTAGATGAGGTGGCCCTTTCGGGAGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 441 ACCTACTCCTAGATGAGGTGGCCCTTTCGGGAGAGCTGCTCTGCAAGCTGGTGCACTTC 500
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 360
Db 501 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 560
Qy 361 TTCTAGGTGTGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 561 TTCTAGGTGTGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
Qy 421 CTGGGACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 621 CTGGGACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
Qy 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGGTATGACATGACACGAGCAAGAAAT 540
Db 681 TCCACACGAGCTACATCAATGGCCAGATGATCTGGTATGACATGACACGAGCAAGAAAT 740
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 741 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
Qy 601 GGTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 801 GGTCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 860
Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGGACCATCTCTACTGCTGCTGCTG 720
Db 861 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGGACCATCTCTACTGCTGCTGCTG 920
Qy 721 CCTCTTCAACCTCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 921 CCTCTTCAACCTCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
Qy 781 CTTTCTGCTTCTCAGACCTGCCAGCTCTTGTATGGCAGCAGGTGTGCTGCTGCTGCTGCTGCTG 840
Db 981 CTTTCTGCTTCTCAGACCTGCCAGCTCTTGTATGGCAGCAGGTGTGCTGCTGCTGCTGCTGCTG 1040
Qy 841 GAGGCTCTGCTGAGTGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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Db 1041 GAGGCTCTGGTGTGAGCAGCTGCTCAACCCAGCTCTGTACTTCTTTCAAGGG 1100
Qy 901 GGC AAAATAGCTCAGCTCTCTCAGAACTGAGGCAAGCAAGTTGGGTGAGCATCCA 960
Db 1101 GGC AAAATAGAGTCAGCTCTCTCAGAACTGAGGCAAGCAAGTTGGGTGAGCATCCA 1160
Qy 961 GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1002
Db 1161 GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1202

RESULT 3

US-10-292-798-619
; Sequence 619, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 619
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1334)
; NAME/KEY: CDS
; LOCATION: (201)..(715)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(1134)
US-10-292-798-619

Query Match 99.8%; Score 1000.4; DB 6; Length 1334;

Best Local Similarity 99.9%; Pred. No. 9.2e-303;

Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGAGGTGGACATGAATACATCAGGAAAGGTCTCTGCCAGTTCTCAGAGAG 60
Db 201 ATGGAGAGGTGGACATGAATACATCAGGAAAGGTCTCTGCCAGTTCTCAGAGAG 260
Qy 61 TACAAGCAAGTCTACTCTCTCGCTTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db 261 TACAAGCAAGTCTACTCTCTCGCTTACAGTATCATCTTTATCTAGGCTGCCACTA 320
Qy 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACACC 180
Db 321 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACACC 380
Qy 181 TATCTGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATC 240
Db 381 TATCTGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATC 440
Qy 241 ACCTACTCAGTAGAGAGAGTGGCCCTTCTGGGGAGCTGCTGCAAGCTGGTGCACTTC 300
Db 441 ACCTACTCAGTAGAGAGAGTGGCCCTTCTGGGGAGCTGCTGCAAGCTGGTGCACTTC 500
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCTGACCTGCATCTCTGTGACCCAG 360
Db 501 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCTGACCTGCATCTCTGTGACCCAG 560

Qy 361 TTCTAGTGTGTGCCACCTGTTGCTGCTGCCCTACCGGACCCGAGGATGCTCCCTGG 420
Db 561 TTCTAGTGTGTGCCACCTGTTGCTGCTGCCCTACCGGACCCGAGGATGCTCCCTGG 620
Qy 421 CTGGGCACAGCACCACCTGGGCCCTGGTGTCTCTCCAGCTGCTGCCACACTGGCCTTC 480
Db 621 CTGGGCACAGCACCACCTGGGCCCTGGTGTCTCTCCAGCTGCTGCCACACTGGCCTTC 680
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGAGAAAT 540
Db 681 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGAGAAAT 740
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600
Db 741 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 800
Qy 601 GGTCAATTTTGGTGTCTATTCTCACTGATGGTCAGGAGCTGATCAAGCCAGAGGAGAACT 660
Db 801 GGTCAATTTTGGTGTCTATTCTCACTGATGGTCAGGAGCTGATCAAGCCAGAGGAGAACT 860
Qy 861 CATGAGACAGGCAACACAGCCGAGCAGGTCCATCCGAGCCATCTCTACTGGTGTGG 720
Db 920 CATGAGACAGGCAACACAGCCGAGCAGGTCCATCCGAGCCATCTCTACTGGTGTGG 920
Qy 721 CCTCTTCACTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCTACCTCACCACCTG 780
Db 921 CCTCTTCACTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCTACCTCACCACCTG 980
Qy 781 CTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTGAGCAGCTGCTCAACCCAGTCTCTTCAAGGG 900
Db 981 CTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTGAGCAGCTGCTCAACCCAGTCTCTTCAAGGG 1100
Qy 901 GGC AAAATAGTCAAGCTCTCTCAGAACTGAGGCAAGCAAGTTGGGTGAGCATCCA 960
Db 1101 GGC AAAATAGTCAAGCTCTCTCAGAACTGAGGCAAGCAAGTTGGGTGAGCATCCA 1160
Qy 961 GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1002
Db 1161 GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1202

RESULT 4

US-10-275-910-1

; Sequence 1, Application US/10275910

; Publication No. US20030166142A1

; GENERAL INFORMATION:

; APPLICANT: Ramakrishnan, Shyam

; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR

; FILE REFERENCE: 4974.00885

; CURRENT APPLICATION NUMBER: US/10/275,910

; CURRENT FILING DATE: 2002-11-12

; PRIOR APPLICATION NUMBER: US 60/203,582

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: US 60/269,857

; PRIOR FILING DATE: 2001-02-21

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 3143

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: gene

; LOCATION: (520)..(1373)

US-10-275-910-1

Query Match

Best Local Similarity 99.8%; Score 1000.4; DB 6; Length 3143;

Matches 1001; Conservative 99.9%; Pred. No. 1.3e-302;

Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	ATGAGAGGTGGACATGATATACATACAGGAAACAGGTCCTGCGCATGTTCTCAGAGAAG	60	
Db	520	ATGAGAGGTGGACATGATATACATACAGGAAACAGGTCCTGCGCATGTTCTCAGAGAAG	579	
Qy	61	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTA	120	
Db	580	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTA	639	
Qy	121	AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC	180	
Db	640	AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGTGCCACACC	699	
Qy	181	TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATATGTGTATTTGCCCTTCTCATCATC	240	
Db	700	TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATATGTGTATTTGCCCTTCTCATCATC	759	
Qy	241	ACCTACTCAGTATGACAGTGGCGCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACCTC	300	
Db	760	ACCTACTCAGTATGACAGTGGCGCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACCTC	819	
Qy	301	CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGCATCTCTGTGCACACG	360	
Db	820	CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGCATCTCTGTGCACACG	879	
Qy	361	TTCTAGGTGTGCCACCACTGTGTGGTGGTCCCTACCGGACCCGAGCATGCTCTGG	420	
Db	880	TTCTAGGTGTGCCACCACTGTGTGGTGGTCCCTACCGGACCCGAGCATGCTCTGG	939	
Qy	421	CTGGGACACGACCACTGGGCCCTGGTGTCTCCAGCTGCTGCCACACTGGCCCTC	480	
Db	940	CTGGGACACGACCACTGGGCCCTGGTGTCTCCAGCTGCTGCCACACTGGCCCTC	999	
Qy	481	TCCACACGGAAGTATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGCAAGAAAT	540	
Db	1000	TCCACACGGAAGTATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGCAAGAAAT	1059	
Qy	541	TTTGATCGGCTTTTGGCTACGGCATATGTTCTGACATTTGCTGTGGCTTTTTCCTCCTT	600	
Db	1060	TTTGATCGGCTTTTGGCTACGGCATATGTTCTGACATTTGCTGTGGCTTTTTCCTCCTT	1119	
Qy	601	GGTCATTTTGGTGTCTATTCACATGATGGTTCAGGAGCTGATCAAGCCAGAGGAGACCT	660	
Db	1120	GGTCATTTTGGTGTCTATTCACATGATGGTTCAGGAGCTGATCAAGCCAGAGGAGACCT	1179	
Qy	661	CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGAGACCATCCTACTGTGTGTGG	720	
Db	1180	CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGAGACCATCCTACTGTGTGTGG	1239	
Qy	721	CCTCTTCAACCTCTGTTTGTGGCTTCCATATACATCGCTCTTCTACTCCACATCTG	780	
Db	1240	CCTCTTCAACCTCTGTTTGTGGCTTCCATATACATCGCTCTTCTACTCCACATCTG	1299	
Qy	781	CTTTCTGCTTCTCAGACCTGCAGCTTTGATGGAGCCAGTGTGGCTTACAGATATG	840	
Db	1300	CTTTCTGCTTCTCAGACCTGCAGCTTTGATGGAGCCAGTGTGGCTTACAGATATG	1359	
Qy	841	GAGGCTCTGGTGTGTGAGCAGCTGCTCAACCCAGTCTCTGCTTCTTTCAAGGGG	900	
Db	1360	GAGGCTCTGGTGTGTGAGCAGCTGCTCAACCCAGTCTCTGCTTCTTTCAAGGGG	1419	
Qy	901	GGCAAAATAGAGTCAAGCTCTCCAGAACTGAGGAGCAAGATTTGGGTGAGCATCCA	960	
Db	1420	GGCAAAATAGAGTCAAGCTCTCCAGAACTGAGGAGCAAGATTTGGGTGAGCATCCA	1479	
Qy	961	GCTGGGAGGAGAGATGCCAGGTTGAACAGATCTCGGTTAA	1002	
Db	1480	GCTGGGAGGAGAGATGCCAGGTTGAACAGATCTCGGTTAA	1521	

RESULT 5

US-10-023-586B-1

; Sequence 1, Application US/10023586B
; Publication No. US2003016882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (BP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US2003016882A1el Polypeptide
; FILE REFERENCE: PC10960AGPR
; CURRENT APPLICATION NUMBER: US/10/023,586B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-586B-1

Query Match 99.4%; Score 996.4; DB 6; Length 1082; Best Local Similarity 99.9%; Pred. No. 1.5e-301; Matches 997; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	ATGAGAGGTGGACATGATATACATACAGGAAACAGGTCCTGCGCATGTTCTCAGAGAAG	60	
Db	85	ATGAGAGGTGGACATGATATACATACAGGAAACAGGTCCTGCGCATGTTCTCAGAGAAG	144	
Qy	61	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTA	120	
Db	145	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTA	204	
Qy	121	AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC	180	
Db	205	AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC	264	
Qy	181	TATCTGTGTAACCTGATGGTGGCGACCTGCTTTATGTGTCTATTGCCCTTCTCATCATC	240	
Db	265	TATCTGTGTAACCTGATGGTGGCGACCTGCTTTATGTGTCTATTGCCCTTCTCATCATC	324	
Qy	241	ACCTACTCACTAGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATTC	300	
Db	325	ACCTACTCACTAGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATTC	384	
Qy	301	CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGTCATCTCTGTGCACAG	360	
Db	385	CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGTCATCTCTGTGCACAG	444	
Qy	361	TTCTTAGTGTGTGGCCACCCACTGTGTTCCCTACCGACCCGAGCATGCTCTGG	420	
Db	445	TTCTTAGTGTGTGGCCACCCACTGTGTTCCCTACCGACCCGAGCATGCTCTGG	504	
Qy	421	CTGGGACACGACCACTCTGGGGCCCTGGTGGTCTCCAGCTGTGCTGCCACACTGGCCTTC	480	
Db	505	CTGGGACACGACCACTCTGGGGCCCTGGTGGTCTCCAGCTGTGCTGCCACACTGGCCTTC	564	
Qy	481	TCCACACGGAAGTATCAATGGCAGATGATCTGGTATGACATGACAGCCAGCAAGAAAT	540	
Db	565	TCCACACGGAAGTATCAATGGCAGATGATCTGGTATGACATGACAGCCAGCAAGAAAT	624	
Qy	541	TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCCTT	600	
Db	625	TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCCTT	684	
Qy	601	GGTCATTTTGGTGTGCTATTCTACTGATGGTCAGGAGCTTGATCAAGCCAGAGGAGAACT	660	
Db	685	GGTCATTTTGGTGTGCTATTCTACTGATGGTCAGGAGCTTGATCAAGCCAGAGGAGAACT	744	


```
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 165
; LENGTH: 1108
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-165
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Query Match 97.5%; Score 977.4; DB 7; Length 1108;
Best Local Similarity 99.7%; Pred. No. 1.4e-295;
Matches 1000; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 ATGAGAGAGGTGGACATGAATACATACAGGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 96 ATGAGAGAGGTGGACATGAATACATACAGGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 155

Qy 61 TACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 156 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 215

Qy 121 AATGGCACTGTTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACCACC 180
Db 216 AATGGCACTGTTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACCACC 275

Qy 181 TATCTGGTGAACCTGTAGTGGCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 240
Db 276 TATCTGGTGAACCTGTAGTGGCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 335

Qy 241 ACCTACTACTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 336 ACCTACTACTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 395

Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTCATCTCTGTGCAACAG 360
Db 396 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTCATCTCTGTGCAACAG 455

Qy 361 TTCTTAGGTGTGCCACCACTGTTGTGCTGCTTACCGGACCCGACGCAATGCTCTGG 420
Db 456 TTCTTAGGTGTGCCACCACTGTTGTGCTGCTTACCGGACCCGACGCAATGCTCTGG 515
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RESULT 8

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US-09-885-453-3
; Sequence 3, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCR $\alpha$ 10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DNA sequence
; LOCATION: (1)..(1017)
; OTHER INFORMATION: GPCR $\alpha$ 6 DNA sequence
US-09-885-453-3
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Query Match 91.9%; Score 920.4; DB 3; Length 1017;
Best Local Similarity 99.8%; Pred. No. 1e-277;
Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ATGAGAGAGGTGGACATGAATATCATCAGGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 85 ATGAGAGAGGTGGACATGAATATCATCAGGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 144
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Qy 61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCTTAGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCTTAGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACT 180
Db 205 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACT 264
Qy 181 TATCTGTGTGAACCTGTGGTGGCGACCTGTCTTTATGTGCTATTGGCTTCTCTCATCATC 240
Db 265 TATCTGTGTGAACCTGTGGTGGCGACCTGTCTTTATGTGCTATTGGCTTCTCTCATCATC 324
Qy 241 ACCTACTCACTAGATGACAGGTGGCCCTTCCAGCTGTCTTCCAGAGCTGGTGCACCTTC 300
Db 325 ACCTACTCACTAGATGACAGGTGGCCCTTCCAGAGCTGGTGCACCTTC 384
Qy 301 CTGTTCTATATCAACCTTTACGGGAGCATCTGTCTGTGACCTGATCTCTGTGCACGAG 360
Db 385 CTGTTCTATATCAACCTTTACGGGAGCATCTGTCTGTGACCTGATCTCTGTGCACGAG 444
Qy 361 TTCCTAGGTGTGGCCACCACTGTGTGGTGGCGACCTGTACCGGACCCGAGGATGCTGTGG 420
Db 445 TTCCTAGGTGTGGCCACCACTGTGTGGTGGCGACCTGTACCGGACCCGAGGATGCTGTGG 504
Qy 421 CTGGGCAACGACCACTGTGGTGGCGACCTGTGTGGTGGCGACCTGTGTGGTGGCGACCT 480
Db 505 CTGGGCAACGACCACTGTGGTGGCGACCTGTGTGGTGGCGACCTGTGTGGTGGCGACCT 564
Qy 481 TCCCAACGAGGACTACATCAATGAGGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 565 TCCCAACGAGGACTACATCAATGAGGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 624
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATGTCTGAGCTTCTTCCCTCCTT 600
Db 625 TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATGTCTGAGCTTCTTCCCTCCTT 683
Qy 601 GGTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 684 GGTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 743
Qy 661 CATGAGGACAGGCAACACAGCCGAGCGAGGTCCATCCGGACCACTCTTACTCTACCATCTG 720
Db 744 CATGAGGACAGGCAACACAGCCGAGCGAGGTCCATCCGGACCACTCTTACTCTACCATCTG 923
Qy 841 GAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 924 GAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 983
Qy 901 GGCAGGCAATAGAGTCAAGCTCTCTCAGAACTGA 934
Db 984 GGCAGGCAATAGAGTCAAGCTCTCTCAGAACTGA 1017
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RESULT 9

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US-10-079-384-5
; Sequence 5, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
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; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1017)
; OTHER INFORMATION:
US-10-079-384-5
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Query Match 91.9%; Score 920.4; DB 5; Length 1017;
Best Local Similarity 99.8%; Pred. No. 1e-277;
Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Qy 1 ATGGAGAAGGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAA 60
Db 85 ATGGAGAAGGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAA 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCTTAGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCTTAGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCA 180
Db 205 AATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCA 264
Qy 181 TATCTGTGTGAACCTGTGTGGCGACCTGTCTTTATGTGCTATTGTGCTTCTCTCATCATC 240
Db 265 TATCTGTGTGAACCTGTGTGGCGACCTGTCTTTATGTGCTATTGTGCTTCTCTCATCATC 324
Qy 241 ACCTACTCACTAGATGACAGGTGGCCCTTCCAGCTGTCTTCCAGAGCTGGTGCACCTTC 300
Db 325 ACCTACTCACTAGATGACAGGTGGCCCTTCCAGAGCTGGTGCACCTTC 384
Qy 301 CTGTTCTATATCAACCTTTACGGGAGCATCTGTCTGTGACCTGATCTCTGTGCACGAG 360
Db 385 CTGTTCTATATCAACCTTTACGGGAGCATCTGTCTGTGACCTGATCTCTGTGCACGAG 444
Qy 361 TTCCTAGGTGTGGCCACCACTGTGTGGTGGCGACCTGTACCGGACCCGAGGATGCTGTGG 420
Db 445 TTCCTAGGTGTGGCCACCACTGTGTGGTGGCGACCTGTACCGGACCCGAGGATGCTGTGG 504
Qy 421 CTGGGCAACGACCACTGTGGTGGCGACCTGTGTGGTGGCGACCTGTGTGGTGGCGACCT 480
Db 505 CTGGGCAACGACCACTGTGGTGGCGACCTGTGTGGTGGCGACCTGTGTGGTGGCGACCT 564
Qy 481 TCCCAACGAGGACTACATCAATGAGGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 565 TCCCAACGAGGACTACATCAATGAGGAGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 624
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATGTCTGAGCTTCTTCCCTCCTT 600
Db 625 TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATGTCTGAGCTTCTTCCCTCCTT 683
Qy 601 GGTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 684 GGTCAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 743
Qy 661 CATGAGGACAGGCAACACAGCCGAGCGAGGTCCATCCGGACCACTCTTACTCTACCATCTG 720
Db 744 CATGAGGACAGGCAACACAGCCGAGCGAGGTCCATCCGGACCACTCTTACTCTACCATCTG 803
Qy 721 CCTCTTCAACCTCTGTGTGTGGCCCTTCCATATCATCTGCTCTTACTCTACCATCTG 780
Db 804 CCTCTTCAACCTCTGTGTGTGGCCCTTCCATATCATCTGCTCTTACTCTACCATCTG 863
Qy 781 CTTTCTGCTTCTCAGGACTGCGACCTTTCATGGCAGCCAGTGTGGCTTACAGATATG 840
Db 864 CTTTCTGCTTCTCAGGACTGCGACCTTTCATGGCAGCCAGTGTGGCTTACAGATATG 923
Qy 841 GAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 924 GAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 983
Qy 901 GGCAGGCAATAGAGTCAAGCTCTCTCAGAACTGA 934
Db 984 GGCAGGCAATAGAGTCAAGCTCTCTCAGAACTGA 1017
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Db 924 GAGCCCTCTGTGTAGTGTGACAGCTGCTCAACCCAGTCTCTGTACTTCTTTCAAGGG 983
Qy 901 GGCAAAATAGATGAGTCAGGCTCTCTCCAGAAACTGA 934
Db 984 GGCAAAATAGATGAGTCAGGCTCTCTCCAGAAACTGA 1017
RESULT 10
US-10-023-586B-3
; Sequence 3, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (EP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US20030166882A1e1 Polypeptide
; FILE REFERENCE: PC10960AGR
; CURRENT APPLICATION NUMBER: US/10/023,586B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-586B-3

Query Match ; 91.5%; Score 917.2; DB 6; Length 1020;
Best Local Similarity 99.5%; Pred. No. 1.1e-276;
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
Qy 1 ATGAGAAAGTGGACATGAAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAG 60
Db 85 ATGAGAAAGTGGACATGAAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAG 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180
Db 205 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 264
Qy 181 TATCTGTGAACCTGATGGTGGCGACCTGCTTTATGTCTATTGCCCTTCTCTCATCATC 240
Db 265 TATCTGTGAACCTGATGGTGGCGACCTGCTTTATGTCTATTGCCCTTCTCTCATCATC 324
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATTC 300
Db 325 ACCTACTCACTAGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATTC 384
Qy 301 CTGTTCTATATCAACCTTTAGCGGACGATCTCTGCTGACCTGCTGCTGTGCCACGAG 360
Db 385 CTGTTCTATATCAACCTTTAGCGGACGATCTCTGCTGACCTGCTGCTGTGCCACGAG 444
Qy 361 TTCTCTAGTGTGTGCCACCACTGTTTGGCTGCGCTACCGGACCCGACGATGCGCTGG 420
Db 445 TTCTCTAGTGTGTGCCACCACTGTTTGGCTGCGCTACCGGACCCGACGATGCGCTGG 504
Qy 421 CTGGGCAACGACCACTGCGGCCCTGTGGTCTCCAGCTGTGCCACACTGGCCCTTC 480
Db 505 CTGGGCAACGACCACTGCGGCCCTGTGGTCTCCAGCTGTGCCACACTGGCCCTTC 564
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCCAGCAAGAAAT 540

Db 565 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCGCAAGAAAT 624
Qy 541 TTTGATCGGCTTTTGGCTACGGCAGTAGTTCTGACATTGTCTGGCTTTCTTTT--CCCTCC 598
Db 625 TTTGATCGGCTTTTGGCTACGGCAGTAGTTCTGACATTGTCTGGCTTTCTTTTCCCTCC 684
Qy 599 TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAAC 658
Db 685 TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAAC 744
Qy 659 CTGATGAGGACAGCAACAGCCCGAGCCAGGTCCATCCGGACCATCTTACTTGGTGTGT 718
Db 745 CTGATGAGGACAGCAACAGCCCGAGCCAGGTCCATCCGGACCATCTTACTTGGTGTGT 804
Qy 719 GGCCTCTTACCCCTCTGTTTTGTGCCCCCTCCATATCACTCGCTCTCTTACTCACCATC 778
Db 805 GGCCTCTTACCCCTCTGTTTTGTGCCCCCTCCATATCACTCGCTCTTACTCACCATC 864
Qy 779 TGCTTTCTGCTTTCTCAGGACTGCGAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA 838
Db 865 TGCTTTCTGCTTTCTCAGGACTGCGAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA 924
Qy 839 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTCTTCAAGG 898
Db 925 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTCTTCAAGG 984
Qy 899 GGGGCAAAATAGAGTCAGGCTCTCTCCAGAAACTGA 934
Db 985 GGGGCAAAATAGAGTCAGGCTCTCTCCAGAAACTGA 1020

RESULT 11
US-10-763-972-3
; Sequence 3, Application US/10763972
; Publication No. US20040137500A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: Novel Polypeptide
; FILE REFERENCE: PC10960B
; CURRENT APPLICATION NUMBER: US/10/763,972
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-763-972-3

Query Match 91.5%; Score 917.2; DB 7; Length 1020;
Best Local Similarity 99.5%; Pred. No. 1.1e-276;
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
Qy 1 ATGAGAAAGTGGACATGAAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAG 60
Db 85 ATGAGAAAGTGGACATGAAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAG 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTAGGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTAGGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180

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Db 205 AATGGCACTGCTTGTGGCACTCTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACC 264
Qy 181 TATCTGTGAACCTGATGGTGGCGACCTGTTTATGTGCTATTGGCTTATGGCTTCTCATCATC 240
Db 265 TATCTGTGAACCTGATGGTGGCGACCTGTTTATGTGCTATTGGCTTATGGCTTCTCATCATC 324
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCACTAGATGACAGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG 360
Db 385 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG 444
Qy 361 TTCCTAGTGTGTGCCACCACTGTTTCGCTGCTCCCTACCGACCCGCGAGCATGCCCTGG 420
Db 445 TTCCTAGTGTGTGGCACCACTGTTTCGCTGCTCCCTACCGACCCGCGAGCATGCCCTGG 504
Qy 421 CTGGCACACGACCACTGGGCCCTGGTGGTCTCTCCAGCTGCTGCCACACTGGCCCTTC 480
Db 505 CTGGCACACGACCACTGGGCCCTGGTGGTCTCTCCAGCTGCTGCCACACTGGCCCTTC 564
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAAAT 540
Db 565 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAAAT 624
Qy 541 TTTGATCGGCTTTTGGCTACGGATAGTTCTGACATGTTCTGGCTTCTTTT--CCCTCC 598
Db 625 TTTGATCGGCTTTTGGCTACGGATAGTTCTGACATGTTCTGGCTTCTTTTCCCTCC 684
Qy 599 TTGTCATTTTGGTGTGCTATTCTAGTATGTCAGGAGCCTGATCAAGCCAGAGAGAAC 658
Db 685 TTGTCATTTTGGTGTGCTATTCTAGTATGTCAGGAGCCTGATCAAGCCAGAGAGAAC 744
Qy 659 CTGATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCACTCTACTGGTGTG 718
Db 745 CTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCACTCTACTGGTGTG 804
Qy 719 GGCCTTTCACCTCTGTTTGTGGCTTTCATATCACTGCTCTGCTTCTACTCACCATC 778
Db 805 GGCCTTTCACCTCTGTTTGTGGCTTTCATATCACTGCTCTGCTTCTACTCACCATC 864
Qy 779 TGCCTTTCGCTTCTCAGGAGTGCAGCTCTTGTATGGCAGCAGTGTGGCTTACAAGATA 838
Db 865 TGCCTTTCGCTTCTCAGGAGTGCAGCTCTTGTATGGCAGCAGTGTGGCTTACAAGATA 924
Qy 839 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCCCTGATCTTTTCAAGG 898
Db 925 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCCCTGATCTTTTCAAGG 984
Qy 899 GGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 934
Db 985 GGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 1020
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RESULT 12

US-10-333-946-20

; Sequence 20, Application US/10333946

; Publication No. US20040023252A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.

; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.

; APPLICANT: BURFORD, Neil; YUE, Henry

; APPLICANT: GANDHI, Aneena R.; ELLIOTT, Vicki S.

; APPLICANT: RAMKUMAR, Javalaxmi; BAUGHN, Mariah R.

; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.

; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.

; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.

; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam

; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.

; APPLICANT: LEE, Ernestine A.; DING, Li

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: P1-0176 USN

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; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CB1
; US-10-333-946-20
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Query Match 91.5%; Score 917.2; DB 7; Length 1076;

Best Local Similarity 99.5%; Pred. No. 1.1e-276;

Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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Qy 1 ATGAGAAGGTGGAGCATGAATACATCAGAGAACAGGTCTCTGCGAGTTCTCAGAGAAG 60
Db 141 ATGAGAAGGTGGAGCATGAATACATCAGAGAACAGGTCTCTGCGAGTTCTCAGAGAAG 200
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db 201 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTAGGCTGCCACTA 260
Qy 121 AATGGCACTGCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACCAACC 180
Db 261 AATGGCACTGCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACCAACC 320
Qy 181 TATCTGTGAACCTGATGGTGGCGCACTGCTGTTTATGTGCTATTGCCCTTCTCATCATC 240
Db 321 TATCTGTGAACCTGATGGTGGCGCACTGCTGTTTATGTGCTATTGCCCTTCTCATCATC 380
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 381 ACCTACTCACTAGATGACAGTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 440
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGCATCTCTGTGCACAG 360
Db 441 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGCATCTCTGTGCACAG 500
Qy 361 TTCCTAGTGTGTGCCACCACTGTTGCTGGCTTACCGGACCCGCGAGCATGCCCTGG 420
Db 501 TTCCTAGTGTGTGCCACCACTGTTGCTGGCTTACCGGACCCGCGAGCATGCCCTGG 560
Qy 421 CTGGGCAACGACCACTGGGCCCTGGTGGTCTCCAGCTGCTGCCACACTGGCCCTTC 480
Db 561 CTGGGCAACGACCACTGGGCCCTGGTGGTCTCCAGCTGCTGCCACACTGGCCCTTC 620
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAAAT 540
Db 621 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAAAT 680
Qy 541 TTTGATCGGCTTTTGGCTACGGATAGTTCTGACATGTTCTGGCTTCTTTT--CCCTCC 598
Db 681 TTTGATCGGCTTTTGGCTACGGATAGTTCTGACATGTTCTGGCTTCTTTTCCCTCC 740
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Qy 599 TTGTCATTTTGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAAC 658
Db |||||||
Qy 741 TTGTCATTTTGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAAC 800
Db |||||||
Qy 659 CTATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACATCCTACTGGTGTG 718
Db |||||||
Qy 801 CTATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACATCCTACTGGTGTG 860
Db |||||||
Qy 719 GGCCTCTTCAACCTCTCTGTTTGTGCTTCCATATCACTCGCTCTCTTCACTCAACATC 778
Db |||||||
Qy 861 GGCCTCTTCAACCTCTCTGTTTGTGCTTCCATATCACTCGCTCTCTTCACTCAACATC 920
Db |||||||
Qy 779 TGCCTTCTGCTTCTCAGGACTCCAGCTCTTGATGCGCAGCCAGTGGGCTCAAGATA 838
Db |||||||
Qy 921 TGCCTTCTGCTTCTCAGGACTCCAGCTCTTGATGCGCAGCCAGTGGGCTCAAGATA 980
Db |||||||
Qy 839 TGAAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTTCAAGG 898
Db |||||||
Qy 981 TGAAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTTCAAGG 1040
Db |||||||
Qy 899 GGGCAAAATAGAGTCAGGCTCTCCAGAAACTGA 934
Db |||||||
Qy 1041 GGGCAAAATAGAGTCAGGCTCTCCAGAAACTGA 1076
Db |||||||
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RESULT 13

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US-10-275-910-6
; Sequence 6, Application US/10275910
; Publication No. US20030166142A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 4974.00885
; CURRENT APPLICATION NUMBER: US/10/275,910
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2000-05-11
; PRIOR FILING DATE: 2000-05-11
; PRIOR FILING DATE: 2000-05-11
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 851
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-275-910-6
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Query Match 84.8%; Score 849.4; DB 6; Length 851;
Best Local Similarity 99.9%; Pred. No. 1.9e-255;
Matches 850; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 ATGGAAGGTGGACATGATATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db |||||||
Qy 1 ATGGAAGGTGGACATGATATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db |||||||
Qy 61 TACAGGAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db |||||||
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db |||||||
Qy 121 AATGGCACTGCTTGTGGCACTCTCTGGGCGCAACCAAGGCTGGAGCTGTGCCACCACC 180
Db |||||||
Qy 121 AATGGCACTGCTTGTGGCACTCTCTGGGCGCAACCAAGGCTGGAGCTGTGCCACCACC 180
Db |||||||
Qy 181 TATCTGTGAACCTGATGTTGGCCGACCTGTTTATGTGCTATTGCTTATGCTTCTCATCATC 240
Db |||||||
Qy 181 TATCTGTGAACCTGATGTTGGCCGACCTGTTTATGTGCTATTGCTTATGCTTCTCATCATC 240
Db |||||||
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTGGGAGCTGCTCTGCAAGCTGGTGCATTC 300
Db |||||||
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTGGGAGCTGCTCTGCAAGCTGGTGCATTC 300
Db |||||||
Qy 301 CTGTTCTATATCAACCTTTTACGGCAGCATCTGCTGCTGACCTCATCTCTGTGSCACAG 360
Db |||||||
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Db 301 CTGTTCTATATCAACCTTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGACACAG 360
Qy |||||||
Qy 361 TTCTTAGTGTGTGGCCACCCACTGTGTTGCTGCCCTTACCGGACCCGACGCAATGCCCTGG 420
Db |||||||
Qy 361 TTCTTAGTGTGTGGCCACCCACTGTGTTGCTGCCCTTACCGGACCCGACGCAATGCCCTGG 420
Db |||||||
Qy 421 CTGGGACACAGCACCCTGGGCCCCTGCTCCAGCTGCTGCCACACACTGGCCCTTC 480
Db |||||||
Qy 421 CTGGGACACAGCACCCTGGGCCCCTGCTCCAGCTGCTGCCACACACTGGCCCTTC 480
Db |||||||
Qy 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGGTATGACATGACACGACCAAGAGAAT 540
Db |||||||
Qy 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGGTATGACATGACACGACCAAGAGAAT 540
Db |||||||
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGTCGCTTCTTTCCCTCCTT 600
Db |||||||
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGTCGCTTCTTTCCCTCCTT 600
Db |||||||
Qy 601 GGTCAATTTTGGTGTGCTATTCTGATGGTCAGAGCCTGATCAAGCCAGAGGAACCT 660
Db |||||||
Qy 601 GGTCAATTTTGGTGTGCTATTCTGATGGTCAGAGCCTGATCAAGCCAGAGGAACCT 660
Db |||||||
Qy 661 CATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCATCTCTACTGTGTGG 720
Db |||||||
Qy 661 CATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCATCTCTACTGTGTGG 720
Db |||||||
Qy 721 CCTCTTCAACCTCTGTTTGTGCCCCTTCATATCACTGCTCTTCTTACCTCACCATCTG 780
Db |||||||
Qy 721 CCTCTTCAACCTCTGTTTGTGCCCCTTCATATCACTGCTCTTCTTACCTCACCATCTG 780
Db |||||||
Qy 781 CTCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCCTTACAAGATATG 840
Db |||||||
Qy 781 CTCTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCCTTACAAGATATG 840
Db |||||||
Qy 841 GAGGCTCTGG 851
Db |||||||
Qy 841 GAGGCTCTGG 851
Db |||||||
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RESULT 14

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US-10-275-910-4
; Sequence 4, Application US/10275910
; Publication No. US20030166142A1
; GENERAL INFORMATION:
; APPLICANT: Ramakrishnan, Shyam
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 4974.00885
; CURRENT APPLICATION NUMBER: US/10/275,910
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2000-05-11
; PRIOR FILING DATE: 2000-05-11
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 850
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-275-910-4
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Query Match 84.7%; Score 848.4; DB 6; Length 850;
Best Local Similarity 99.9%; Pred. No. 3.8e-255;
Matches 849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 ATGGAAGGTGGACATGATATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db |||||||
Qy 1 ATGGAAGGTGGACATGATATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db |||||||
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCTTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db |||||||
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCTTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db |||||||
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Qy 121 AATGGCACTGCTGTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGGCCACCAAC 180
Db 121 AATGGCACTGCTGTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGGCCACCAAC 180
Qy 181 TATCTGTGTAACCTGATGAGTGGCGAAGCTGTTTATGTTGCTATTTGCTTCTCTCATCATC 240
Db 181 TATCTGTGTAACCTGATGAGTGGCGAAGCTGTTTATGTTGCTATTTGCTTCTCTCATCATC 240
Qy 241 ACCTACTACCTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTCAAGCTGGTGCACTTC 300
Db 241 ACCTACTACCTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTCAAGCTGGTGCACTTC 300
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGATCTCTGTGCAACAG 360
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGATCTCTGTGCAACAG 360
Qy 361 TTCTTAGTGTGGCCACCACTGTTTGTGCTGCTTACCGGACCCGAGGACATGCTCTGG 420
Db 361 TTCTTAGTGTGGCCACCACTGTTTGTGCTGCTTACCGGACCCGAGGACATGCTCTGG 420
Qy 421 CTGGGACCAACCACTGGGCGCTGGTGGTCTCCAGCTGCTGCCACACTGGCCTTC 480
Db 421 CTGGGACCAACCACTGGGCGCTGGTGGTCTCCAGCTGCTGCCACACTGGCCTTC 480
Qy 481 TCCACACGGAATACATCAATGGCCAGATGATCTGGTATGATGACATGACCAAGAGAAAT 540
Db 481 TCCACACGGAATACATCAATGGCCAGATGATCTGGTATGATGACATGACCAAGAGAAAT 540
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCCTT 600
Db 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCCTT 600
Qy 601 GGTCAATTTGTGTGCTATTCACTGATGCTCAGAGCTGATCAAGCCAGAGGAACT 660
Db 601 GGTCAATTTGTGTGCTATTCACTGATGCTCAGAGCTGATCAAGCCAGAGGAACT 660
Qy 661 CATGAGACAGGCAACACAGCCGAGCGAGTCCATCCGAGCACTCTACTGTGTGTGG 720
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RESULT 15

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; Sequence 1747, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1747
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.

BD095704

BD095704.1 GI:22641292

WO 0148188-A/16.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 1002)

Matsumoto,S., Oda,T., Saito,Y., Noriyuki, Morikawa, Yoshida,K.,

Suwa,M., Sugiyama,T., Kishimoto,T., Kanzaki,K., Yasuda,S. and

Inoue,Y.

Novel guanosine triphosphate-bound protein-coupled receptors and

genes encoding them, and their production and use

Patent: WO 0148188-A 16 05-JUL-2001;

HELIIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO

SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU

SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO

YASUDA, YOSHIHISA INOUE

OS Homo sapiens (human)

PN WO 0148188-A/16

PD 05-JUL-2001

PR 28-DEC-2000 WO 2000JP009408

PR 28-DEC-1999 JP 99P 375152,31-MAR-2000 JP 00P 101339 PI

SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI PI

MORIKAWA, KENJI YOSHIDA,

PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI PI

KANZAKI,

PI SHINICHIRO YASUDA, YOSHIHISA INOUE

PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC

C07K16/28

PC C12P21/02, C12Q1/02, C12Q1/68, A61K31/711, A61K48/00, A61P43/00, PC

G01N33/15,

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CC Novel guanosine triphosphate-bound protein-coupled receptors

and genes

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ACCESSION	AJ345013
VERSION	AJ345013.1 GI:34495183
KEYWORDS	nucleoside/nucleotide receptor; P2Y2-like gene.
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
ORGANISM	Hominidae; Homo.
REFERENCE	1
AUTHORS	Bruss, M., Bonisch, H. and Kugelgen, I.
TITLE	Molecular identification and functional characterization of a new G
JOURNAL	protein-coupled nucleoside-/nucleotide receptor
REFERENCE	2 (bases 1 to 1145)
AUTHORS	Bruss, M.
TITLE	Direct Submission
JOURNAL	Submitted (07-SEP-2001) Brussels M., Pharmacology and Toxicology,
JOURNAL	University of Bonn, Reuterstrasse 2 b, D-53113, GERMANY
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ACCESSION AX365511.1 GI:18873666
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Ramakrishnan, S.
AUTHORS
TITLE Regulation of human p2y-like g protein-coupled receptor
JOURNAL Patent: WO 0185764-A 1 15-NOV-2001;
Bayer Aktiengesellschaft (DE)
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AC026960
AC026960.2 GI:7547202
VERSION
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 164502)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collins, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S.,
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
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Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tessfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome

COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 13, 2000 this sequence version replaced gi:7328839.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8491

Center clone name: 170_K_4

----- Summary Statistics

Sequencing vector: MJ3; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 156927 bases at least Q40

Consensus quality: 160376 bases at least Q30

Consensus quality: 161800 bases at least Q20

Insert size: 170000; agarose-fp

Insert size: 163102; sum-of-contigs

Quality coverage: 4.4 in Q20 bases; agarose-fp

Quality coverage: 4.5 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2917: contig of 2917 bp in length
* 2918 3017: gap of 100 bp
* 3018 6310: contig of 3293 bp in length
* 6311 6410: gap of 100 bp
* 6411 9447: contig of 3037 bp in length
* 9448 9547: gap of 100 bp
* 9548 14470: contig of 4923 bp in length
* 14471 14570: gap of 100 bp
* 14571 20528: contig of 5958 bp in length
* 20529 20629: gap of 100 bp
* 20629 24667: contig of 4039 bp in length
* 24668 24767: gap of 100 bp
* 24768 29367: contig of 4600 bp in length
* 29368 29467: gap of 100 bp
* 29468 36237: contig of 6770 bp in length
* 36238 36338: gap of 100 bp
* 36338 46377: contig of 10040 bp in length
* 46378 46477: gap of 100 bp
* 46478 59361: contig of 12884 bp in length
* 59362 59461: gap of 100 bp
* 59462 75221: contig of 15760 bp in length
* 75222 75322: gap of 100 bp
* 75322 93371: contig of 18050 bp in length
* 93372 93471: gap of 100 bp
* 93472 117463: contig of 23992 bp in length
* 117464 117563: gap of 100 bp
* 117564 137715: contig of 20152 bp in length
* 137716 137815: gap of 100 bp
* 137816 164502: contig of 26687 bp in length.

FEATURES
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/db_xref="taxon:9606"
/chromosome="3"
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/clone_lib="RPCI-11 Human Male BAC"
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ORIGIN

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Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 123644 ATGGAGAGGTGGACATGATATACATACAGAACAGGTCTTGCCAGTTCTCAGAGAAG 123585
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db 123584 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGCTGCCACTA 123525

Qy	121	AATGGCACTGTCTGTGGCACTCTCTGGGGCAAACCAAGCGCTGGAGCTGTGCCACCACT	180
Ds	123524	AATGGCACTGTCTGTGGCACTCTCTGGGGCAAACCAAGCGCTGGAGCTGTGCCACCACT	123465
Qy	181	TATCTGTGAAACCTGATGTTGGCGACCTGCTTTATGCTATGCTATGCTTCTCTCATCATC	240
Ds	123464	TATCTGTGAAACCTGATGTTGGCGACCTGCTTTATGCTATGCTATGCTTCTCTCATCATC	123405
Qy	241	ACCTACTACATAGATGACAGTGGCCCTTTCGGGAGCTGCTCTCAAGCTGGTGCATTC	300
Ds	123404	ACCTACTACATAGATGACAGTGGCCCTTTCGGGAGCTGCTCTCAAGCTGGTGCATTC	123345
Qy	301	CTGTTCTATATCAACCTTTACGGAGCATCTGCTGCTGACCTGATCTCTGTGCACCAAG	360
Ds	123344	CTGTTCTATATCAACCTTTACGGAGCATCTGCTGCTGACCTGATCTCTGTGCACCAAG	123285
Qy	361	TTCTAGTGTGTGCCACCACTGTGTTGCTGCTTCCAGGACCGGAGGATGCTGCTGG	420
Ds	123284	TTCTAGTGTGTGCCACCACTGTGTTGCTGCTTCCAGGACCGGAGGATGCTGCTGG	123225
Qy	421	CTGGCACCAGCACCACCTGGGCCCTTGGTGTGCTCTCAGCTGCTGCCACACTGGCCTTC	480
Ds	123224	CTGGCACCAGCACCACCTGGGCCCTTGGTGTGCTCTCAGCTGCTGCCACACTGGCCTTC	123165
Qy	481	TCCACACGGAATCATCAATGGCGAGATGATCTGGTATGATGATGATGATGATGATGAT	540
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Qy	781	CTTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCTTACAGATATG	840
Ds	122864	CTTTCTGCTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCTTACAGATATG	122805
Qy	841	GAGGCTCTGCTGAGTGTGACAGCTGCTCAACCCAGTCTGCTTCTTTTCAAGGGG	900
Ds	122804	GAGGCTCTGCTGAGTGTGACAGCTGCTCAACCCAGTCTGCTTCTTTTCAAGGGG	122745
Qy	901	GGCAAAATAGAGTCAGGCTCTCTCAGAAACTGAGGAGCAACAAAGTTGGGTGAGCATCCA	960
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LOCUS	AC092999	167084 bp	DNA linear PRI 30-JUL-2002
DEFINITION	Homo sapiens 3 BAC RP11-170K4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.		
ACCESSION	AC092999		
VERSION	AC092999.3	GI:19033407	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
	1 (bases 1 to 167084)		
	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,		
	Alsbrooke,S.L., Amarantunga,H.C., Are,J.R., Ayale,M., Banks,T.,		
	Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,		
	Bouck,J., Bowie,S., Briefa,M., Brown,E., Brown,M., Bryant,N.P.,		
	Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,		
	Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,		
	Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,		
	Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,		
	Delaney,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,		
	Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,		
	Douthwaite,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,		
	Earnhart,C., Farguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,		
	Falls,T., Farguto,D., Garcia,A., Garner,T., Garza,N., Gill,R.,		
	Gabisi,A., Gao,J., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,		
	Garrell,J.H., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,		
	Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,		
	Hollins,B., Homei,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,		
	Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,		
	Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,		
	Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,		
	Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,		
	Loulesged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,		
	Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,		
	Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M.,		
	Mei,G., Metsker,M., Miner,G., Miner,Z., Mitchell,T., Monabbat,K.,		
	Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,		
	Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,		
	Nickerson,E., Nwokenwu,S., Ogih,M., Okwuonu,G., Oragunye,N.,		
	Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,M.,		
	Pickens,R., Primus,S., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,		
	Rojas,A., Rojubenok,I., Rolfe,M., Ruiz,S., Savary,G., Scherer,S.,		
	Scott,G., Shen,H., Shostari,N., Sisson,I., Sodergren,E.,		
	Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,		
	Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,		
	Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,		
	Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,		
	Warren,R., Washington,C., Watlington,S., Williams,G.,		
	Williamson,A., Wleczky,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,		
	Wu,Y.F., Zhou,J., Zorrilla,S., Zorrilla,S., Zorrilla,S., Zorrilla,S.,		
	Gibbs,R.		
	Direct Submission		
	Unpublished		
	2 (bases 1 to 167084)		
	Worley,K.C.		
	Direct Submission		
	Submitted (09-AUG-2001) Human Genome Sequencing Center, Department		
	of Molecular and Human Genetics, Baylor College of Medicine, One		
	Baylor Plaza, Houston, TX 77030, USA		
	3 (bases 1 to 167084)		
	Worley,K.C.		
	Direct Submission		
	Submitted (01-MAR-2002) Human Genome Sequencing Center, Department		
	of Molecular and Human Genetics, Baylor College of Medicine, One		
	Baylor Plaza, Houston, TX 77030, USA		
	4 (bases 1 to 167084)		
	Worley,K.C.		
	Direct Submission		
	Submitted (29-MAR-2002) Human Genome Sequencing Center, Department		
	of Molecular and Human Genetics, Baylor College of Medicine, One		
	Baylor Plaza, Houston, TX 77030, USA		
	5 (bases 1 to 167084)		
	Worley,K.C.		
	Direct Submission		
	Submitted (30-JUL-2002) Human Genome Sequencing Center, Department		
	of Molecular and Human Genetics, Baylor College of Medicine, One		
	Baylor Plaza, Houston, TX 77030, USA		
	On Mar 1, 2002 this sequence version replaced gi:18139250.		
	INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email		
	gc-help@bcm.tmc.edu		

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES

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 /db_xref="taxon:9606"
 /chromosome="3"
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 /note="overlaps bases 1. .2005 of clone AC092997"

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complement(997. .1123)
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2422. .2529
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2975. .3004
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complement(5812. .6366)
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Best Local Similarity 99.9%; Pred. No. 5e-239;

Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 161005 ATGGAGAAGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 161064

Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTTATCTAGGCTGCCACTA 120

Db 161065 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTTATCTAGGCTGCCACTA 161124

Qy 121 AATGGCAGCTCTCTTGTGGCACTTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180

Db 161125 AATGGCAGCTCTCTTGTGGCACTTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 161184

Qy 181 TATCTGTGAACCTGATGGTGGCGGACCTGCTTTATGTGCTATGTCCTTCCTCATCATC 240

Db 161185 TATCTGTGAACCTGATGGTGGCGGACCTGCTTTATGTGCTATGTCCTTCCTCATCATC 161244

Qy 241 ACCTACTCACTAGATGACGCTGGCCCTTCGGGAGCTGCTTCTGCAAGCTGGTGCATTC 300

Db 161245 ACCTACTCACTAGATGACGCTGGCCCTTCGGGAGCTGCTTCTGCAAGCTGGTGCATTC 161304

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Db 161305 CTGTTCTTATCAACCTTTACGGCAGCATCCTGCTGCTGCACTGTCATCTCTGTGCAACG 161364

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Db	161365	TTCTAGGTGTGTGCCACCACTGTGTTGGCTTACCGACCGCAGGATGCCTGG	161424	Best Local Similarity	99.9%;	Pred. No. 3.2e-238;		
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QY	541	TTTGATCGGCTTTTGGCTTACGGCACTCTGACATTTGTCTGGCTTTCTTCCCTCCCT	600					
Db	161545	TTTGATCGGCTTTTGGCTTACGGCACTCTGACATTTGTCTGGCTTTCTTCCCTCCCT	161604					
QY	601	GGTCATTTTGGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAACT	660					
Db	161605	GGTCATTTTGGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAACT	161664					
QY	661	CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGACCAATCCCTACTGGTGTGG	720					
Db	161665	CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGACCAATCCCTACTGGTGTGG	161724					
QY	721	CCTCTTACCCCTCTGTTTTGTGGCTTCCATATCACTCGCTCCTTCTACCTCACCATCTG	780					
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QY	781	CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCAGTGTGGCTCAACAGATATG	840					
Db	161785	CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCAGTGTGGCTCAACAGATATG	161844					
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QY	901	GGCAAAATAGAGTCAGGCTCTCAGAAACTGAGGCGAGAACAGTTGGTGAGCATCCA	960					
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QY	961	GCTGGGAGAGAGATGCCAGGTTGAACAGATCTGGGTAA	1002					
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RESULT 8								
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LOCUS		BD187416		PAT 17-JUL-2003				
DEFINITION		Novel polypeptide.						
ACCESSION		BD187416						
VERSION		BD187416.1		GI:32997155				
KEYWORDS		JP 2003009885-A/1.						
SOURCE		Homo sapiens (human)						
ORGANISM		Homo sapiens						
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;						
TITLE		Hominidae; Homo.						
JOURNAL		1 (bases 1 to 1082)						
COMMENT		Fidock, M.D.						
		Novel polypeptide						
		Patent: JP 2003009885-A 1 14-JAN-2003;						
		Pfizer Ltd (EP/GB) only; Pfizer Inc (US JP EP except GB)						
		OS homo sapiens						
		PN JP 2003009885-A/1						
		PD 14-JAN-2003						
		PF 17-DEC-2001 JP 2001382707						
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		mark david fidock						
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Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L3302
Center clone name: 12_N_17
----- Summary Statistics -----
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152766 bases at least Q40
Consensus quality: 158075 bases at least Q30
Consensus quality: 160495 bases at least Q20
Insert size: 17400; agarose-fp
Quality coverage: 162558; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 7254: contig of 7254 bp in length
* 7255: gap of 100 bp
* 7355: 8612: contig of 1258 bp in length
* 8613: 8712: gap of 100 bp
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Qy      121  AATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGAGCTGTGCCACCACC  180
Db      98307 AATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGAGCTGTGCCACCACC  98366

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ACCESSION AX921825
VERSION AX921825.1 GI:40215364
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DEFINITION AF411108
ACCESSION AF411108
VERSION AF411108.1 GI:16566321
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
REFERENCE 1 (bases 1 to 1019)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Discovery and mapping of ten novel G protein-coupled receptor genes
JOURNAL Gene 275 (1), 83-91 (2001)
PUBMED 11574155
REFERENCE 2 (bases 1 to 1019)
AUTHORS Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of
Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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DEFINITION BD187417
ACCESSION BD187417
VERSION BD187417.1 GI:32997156
KEYWORDS JP 2003009885-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1020)
AUTHORS Fidoock,M.D.
TITLE Novel polypeptide
JOURNAL Patent: JP 2003009885-A 2 14-JAN-2003;
Pfizer Ltd (EP/GB only), Pfizer Inc (US JP EP except GB)
COMMENT OS Homo sapiens
PN JP 2003009885-A/2
PD 14-JAN-2003
PF 17-DEC-2001 JP 2001382707
PR 18-DEC-2000 GB 0030855.1,17-JAN-2001 GB 0101222.8 PI
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Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ATGAGAGGTGGACATGATATACATCAGGAACAAGTCTCTGCCAGTTCTTCAGAGAAG 60
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LOCUS
DEFINITION Sequence 3 from Patent EP1215214.
ACCESSION AX458308
VERSION AX458308.1 GI:21725002
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.

REFERENCE	1	Fidock, M.D. Novel polypeptide Patent: EP 1215214-A 3 19-JUN-2002; Pfizer Limited (GB); PFIZER INC. (US) Location/Qualifiers 1. .1020 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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ORIGIN		
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Best Local Similarity	99.5%;	Pred. No. 2.1e-218;
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Qy	61	TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
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Qy	241	ACCTACTACTAGATGACAGTGGCCCTTCCGGAGCTGCTCTGCAAGCTGGTGCATTC 300
Db	325	ACCTACTACTAGATGACAGTGGCCCTTCCGGAGCTGCTCTGCAAGCTGGTGCATTC 384
Qy	301	CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCTATCTCTGTGSCACG 360
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Qy	361	TTCTAGGTGTGGCCACCACTGCTGTGCTGCTTACCGGACCCGCGAGCATGCTGG 420
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Qy	481	TCCACACGCACTACATCAATGGCCAGATGATCTGCTGATGACATGACAGCAAGAGAAT 540
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Db	925	TGGAGGCTCTGGTGTGCTATTCATGATGGTGGAGCTGCTGCTCAACCCAGTCTTCTTCAAGG 984
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RESULT 15
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DEFINITION Sequence 20 from Patent WO0210387.
ACCESSION AX375230
VERSION AX375230.1 GI:19169948
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Thornton, M., Patterson, C., Lal, P., Burford, N., Yue, H., Gandhi, A. R.,
Elliott, V. S., Ramkumar, J., Baughn, M. R., Kallick, D. A., Walla, N. K.,
Hafalia, A. J., Yao, M. G., Lu, Y., Tribouley, C. M., Policky, J. L.,
Kearney, L., Graul, R. C., Warren, B. A. and Ding, L.
G-Protein coupled receptors
TITLE Patent: WO 0210387-A 20 07-FEB-2002;
JOURNAL Incyte Genomics, Inc. (US)
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Best Local Similarity 99.5%; Pred. No. 2.1e-218;
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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Job time : 5419 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
9840.608 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 82156650

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2:*

3: gb_est3:*

4: gb_hic:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_est7:*

9: gb_gss1:*

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11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	226.2	22.6	1138	11 DQ052983	DQ052983 Homo sapi
2	202.2	20.2	2542	4 AK017378	AK017378 Mus muscu
3	202.2	20.2	3001	4 AK005013	AK005013 Mus muscu
4	181.8	18.1	271	10 CD2014932	CD2014932 CH240 511
5	179.2	17.9	693	6 CD217676	CD217676 pgrin.pk0
6	177.2	17.7	1073	11 DQ052984	DQ052984 Pan trogl
7	164.8	16.4	987	10 AY400797	AY400797 Homo sapi
8	164.8	16.4	1425	4 CR624871	CR624871 full-leng
9	164.8	16.4	1515	4 CR612681	CR612681 full-leng
10	164.8	16.4	1532	4 CR618945	CR618945 full-leng
11	164.8	16.4	1564	4 CR626266	CR626266 full-leng
12	164.8	16.4	1589	4 CR626754	CR626754 full-leng
13	164.8	16.4	1592	4 CR605588	CR605588 full-leng
14	164.8	16.4	1594	4 CR606834	CR606834 full-leng
15	164.8	16.4	1638	4 CR617080	CR617080 full-leng
16	164.8	16.4	1651	4 CR597500	CR597500 full-leng
17	164.8	16.4	1686	4 CR626706	CR626706 full-leng
18	164.8	16.4	1890	4 CR598765	CR598765 full-leng
19	163.4	16.3	925	5 BX704227	BX704227 BX704227
20	163.2	16.3	1577	4 CR860841	CR860841 Pongo pyg
21	160.4	16.0	4439	4 AK076364	AK076364 Mus muscu
22	157.2	15.7	810	8 CX444959	CX444959 JGI_XZG10

23	157.2	15.7	987	10 AY400798	AY400798 Pan trogl
24	155.6	15.5	840	8 CX5113496	CX5113496 JGI_XZG57
25	155.4	15.5	802	8 DN025359	DN025359 JGI_CAARS
26	154.8	15.4	639	7 CV028613	CV028613 7176 Full
27	154.8	15.4	643	7 CV030363	CV030363 9460 Full
28	150.4	15.0	987	10 AY400799	AY400799 Mus muscu
29	145.2	14.5	639	6 BQ352828	BQ352828 624212 NC
30	142.8	14.3	641	5 BQ396255	BQ396255 NISC ng19
31	141.8	14.2	627	1 AL675845	AL675845 AL675845
32	141.2	14.1	1090	5 BX397648	BX397648 BX397648
33	140.6	14.0	846	7 CV114223	CV114223 AGENCOURT
34	140.2	14.0	1168	1 AL561864	AL561864 AL561864
35	140	14.0	1023	5 BX332649	BX332649 BX332649
36	138.4	13.8	775	8 DR006403	DR006403 TC109532
37	136.4	13.6	1815	7 CN210812	CN210812 RJA041C08
38	135.2	13.5	1013	4 CR614658	CR614658 full-leng
39	133.2	13.3	470	7 CO959779	CO959779 AGENCOURT
40	131	13.1	1057	5 BX381744	BX381744 BX381744
41	130	13.0	1090	4 CR598708	CR598708 full-leng
42	129.8	13.0	899	5 BQ959110	BQ959110 AGENCOURT
43	127.6	12.7	1035	5 BX379990	BX379990 BX379990
44	127.4	12.7	1042	5 BX397649	BX397649 BX397649
45	127.2	12.7	1095	5 BX358251	BX358251 BX358251

ALIGNMENTS

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LOCUS Homo sapiens P2RY2 gene, VIRTUAL TRANSCRIPT, partial sequence, 1138 bp DNA linear GSS 02-JUN-2005
DEFINITION genomic survey sequence.
ACCESSION DQ052983
VERSION DQ052983.1 GI:66898930
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1138)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1138)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering of them based on alignment. Translation starts at the beginning of alignment.

FEATURES

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Matches 485; Conservative 0; Mismatches 368; Indels 8; Gaps 3;

with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

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DB 616 GTGCTCGGCTGTGCTGAACGCTGCTCTATATCTTCTATGCGGCTCAAAACC 675
QY 163 TGGAGCTGTGCCACCACTATCTGTGACCTGATGTTGGCGGCTCTGTTATGTGCTA 222
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QY 400 CGGACCCGAGGATGCTGCTGGTGCGGACACGACCACTGGCGCTGTGTGCTCTCCAG 459
DB 916 GCGCGGGCCGTTATGCCCGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 975
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QY 520 GACATGACAGCAGCAAGAAATTTGATCGGCTTTTGGCTACGGCATAGTTCTTG--ACAT 577
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QY 758 CGCTCTCTTACCTACCATCTGCTTCTGCTTCTTCTGAGGACTGCCAGCTCTTGTATGCA 817
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QY 818 GCCAGTGGGCTCAAGATATGAGGCTCTGTGTAGTGTGAGCAGTGTGCTCAACCCA 877
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DB 1393 GTACTCTACTTCTGCGCAGG 1413

RESULT 3
AK005013
LOCUS
DEFINITION
Mus musculus adult male liver cDNA, RIKEN full-length enriched
library, clone:1300015C04 product: PURINERGIC RECEPTOR P2Y,
G-PROTEIN COUPLED 2, full insert sequence.
ACCESSION
AK005013
VERSION
AK005013.2 GI:26339698
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayaishizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
2
Carninci, P. and Hayaishizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sunami, I., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayaishizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
(bases 1 to 3001)

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AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, K., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT On Dec 10, 2002 this sequence version replaced gi:12836638. Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCGCAACGCGAGTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGATCAAGAGCTCAATTAATTAACCCGCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.

FEATURES Location/Qualifiers

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 /db_xref="GI:12836639"

 /translation="MAADLEPFWNSTINGWEGDELGVKRFNEDFKVLLPVSYGVVC;VLGLNVALYFLCLKLTWNASTYMFHLVSDLSYASLFLVYVYARGDHPFSTVLCVLFVFLNLYGSLIFLCSVHRCLGVLRPLHSRWRGRVAVRVAVWVWLVLACQAPLVFVTTVSRGTRITCHTDSARELFSHFVAYSSVWMLGLLFAVPFVILVCYVLMARLLKPAYGTGGLPRKRSVPTIALVLAVPALCFPLPFLHRTLYYFSRLDL SCHTLNAINWAYKLTPLASANSCLDPVLYFLAGQRLVRPARDAKPTEPTFPQARR KLGLHPRNRTVRKDLSSVSDSRRTSTPAGSETKDRL"

2982..2987

 /note="putative"

3001

 /note="putative"

polyA_signal

polyA_site

ORIGIN

Query Match 20.2%; Score 202.2; DB 4; Length 3001;
Best local Similarity 54.6%; Pred. No. 2.6e-43;
Matches 470; Conservative 0; Mismatches 383; Indels 8; Gaps 3;
43 TGCAGTTCTCAGAGAAGTACAGCAAGTCTACTCTCCCTGGCCTACAGTATCATCTTT 102

Db 549 TGTGTTTCAACGAGGACTTCAAGTAGTCTGTGTCCTTGTGCGGTGGTGTGC 608

Qy 103 ATCTAGGGCTGGCACCATAATGACACTGTCTTGTGGCAGCTTCTGGGGCCAAACCAAGCGC 162

Db 609 GTGCTGGGTTGTGGCTGGAAGCTGGTCTCTATATCTTCTATGCGCGCTCAAAACC 668

Qy 163 TGGAGCTGTGCCACCACTATCTTGTGGAACCTGANTGTTGGCCGACCTGCTTTATGTGCTA 222

Db 669 TGGAAACGCTCCACCACTACATGTTTCACTGCGGAGTTTTCGGAGCTCTCTCTAGCGACGC 728

Qy 223 T---TGCCCTTCTCATCATCACTACTACTAGTAGACAGGTGGCCCTTTCGGGGAGCTG 279

Db 729 TCCCTGCGCTGTGGTTTATTACTAGCCGGGGTGACCACTGGCCATTTAGCACGGTG 788

Qy 280 CTCTGAAGCTGGTGACCTTCTCTTCTATATCAACCTTTACGGCAGCATCTGCTGCTG 339

Db 789 CTCTGAAGCTGGTGCGTTTCTCTTCTACACCAACCTCTACTGACGATCCTCTTCTC 848

Qy 340 ACCTGCATCTCTGTGCACCAAGTTCTTAGGTGTGTGCCACCACTGTGTTGCTGCCCTAC 399

Db 849 ACCTGCATCAGCGTGCACCGGTGCTGGGAGTCTGTGCGCCTCTGCACCTCCCTGCGTGG 908

Qy 400 CGGACCGGAGGATGCTGCTGGCTGGGCACACGACCACTGGGCCCTGTGGTCTCTCAG 459

Db 909 GGGCGGGCGCTTATGCGCGCGGGTGGCTGGCGGTGTGTGGGTGTGGTGGCTGCG 968

Qy 460 CTGCTGCCACACACTGGCTTCTCCACACAGGACTACATCAATGGCCAGATGATCTGGTAT 519

Db 969 CAGGCACCGTGTCTTACTTGTGCACACAGGCTGGGGGAACCGGATCACTTGGCAT 1028

Qy 520 GACATGACGACCAAGAGAAATTTGATGGCTTTTGGCTTACGGCATATGTTCTG--ACAT 577

Db 1029 GACACCTCGGCCCGAGAGCTCTTTAGCCATTTTGTGGCTTTACAGCTCCGTCATGCTGGGT 1088

Qy 578 TGTCTGGCTTCTTCTCCCTCTGTGTCATTTTGGTGTGCTATTTCATGATGGTTCAGAGC 637

Db 1089 CTGCTTTTGTGCTGCGCTTTTCCGTAATCCTGGTCTGTGTGCTTATGGCCAGCGG 1148

Qy 638 CTGATCAAGCGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATC 697

Db 1149 CTGCTCAACCGCTTATGGGACACAGAGAGGTCTGCTCGGGCCAAAGTCTGTG 1208

Qy 698 CGGACCATCTACTGTGTGTGGCTCTTCCACCTCTGTGTTTGTGGCTTCCATATCACT 757

Db 1209 CGCACCATTCCTTGTGTGCTGCGCGCTTCTGCTCTGCTTCTGCTTCCACCTCAG 1268

Qy 758 CGCTCCCTTCTACCTCACTCTGCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGGCA 817

Db 1269 CGCACCTCTCTACTACTCTTCCGAT---CACTTGACCTAGCTGCCACACCTCAACGCC 1325

Qy 818 GCCAGTGTGGCTTACAGATATGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCCCAACCCA 877

Db 1326 ATCAACATGGCATATAAGATCACCCGCGCTGGCAGCGCAACAGTTGCTTGTGACCCG 1385

Qy 878 GTCTGTATCTTCTTCAAGG 898

Db 1386 GTACTCTACTTCTTGGCAGG 1406

RESULT 4

CZ014932/c 271 bp DNA linear GSS 10-JAN-2005

LOCUS CH240 511J04.TJ CHORI-240 Bos taurus genomic clone CH240_511J04,

DEFINITION genomic survey sequence.

ACCESSION CZ014932

VERSION CZ014932.1 GI:57343493

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 271)
 AUTHORS Costa, J.N., Mota, M. and Caetano, A.R.
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library
 JOURNAL CHORI-240
 COMMENT Unpublished (2003)
 Other_GSSs: CH240_511J04.TV
 Contact: Caetano AR
 Department of Biotechnology
 Embrapa Recursos Geneticos e Biotecnologia
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
 02372, 70770-900 Brasil
 Tel: 55 61 448 4778
 Fax: 55 61 340 3658
 Email: acetano@embrapa.br
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred
 quality value equal to or higher than 20. Bases with quality value
 below 20 were masked with 'N'. For BAC library availability, please
 contact Pieter de Jong (pdejong@mail.cho.org). Clones may be
 purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia
 with financing from Conselho Nacional de Desenvolvimento Cientifico
 e Tecnologico (CNPq), Brazil.
 Plate: 511 row: J column: 04
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 271.
 Location/Qualifiers
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 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="breed: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_511J04"
 /sex="Male"
 /cell_type="Blood"
 /clone_lib="CHORI-240"
 /note="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

FEATURES

source

ORIGIN

Query Match 18.1%; Score 181.8; DB 10; Length 271;
 Best Local Similarity 79.3%; Pred. No. 4.9e-38;
 Matches 214; Conservative 0; Mismatches 53; Indels 3; Gaps 1;
 Qy 184 CTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCT---ATTGCCCTTCTCATCATC 240
 Db |||||
 Qy 270 CTGGGAACCTGATGGTGGCAGATCTGTATNNNNNNNNNNNNNNNNNNNNNNNNNNNN 211
 Db |||||
 Qy 241 ACCTACTCCTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATTC 300
 Db |||||
 Qy 210 ACCTACTCCTGGAGACACCTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGGCTTC 151
 Db |||||
 Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG 360
 Db |||||
 Qy 150 CTGTTCTACGCCAACCTCTACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 91
 Db |||||
 Qy 361 TTCTTAGTGTGTGTCACCACTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 Db |||||
 Qy 90 TTCTTGGGGTGTGTCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
 Db |||||
 Qy 421 CTGGGCACAGCACCACTGGGCCCTGGTG 450
 Db |||||
 Qy 30 NNNNNNNNNACCGCACGTGGGCTCTGGTG 1

RESULT 5

CD217676

LOCUS

DEFINITION pgrin.pk004.g6 Normalized chicken reproductive tract cdna library

linear EST 20-MAY-2003

693 bp mRNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source

(pgrin) Gallus gallus cdna clone pgrin.pk004.g6 5' similar to
 sp|Q98907|PVY3.CHICK.P2Y.purinoreceptor.3 (P2Y3) (Nucleoside
 diphosphate receptor) >emb|CAA66930.1| (X98283) G protein-coupled
 P2 receptor [Gallus gallus], mRNA sequence.
 CD217676
 CD217676.1 GI:30957649
 EST.
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 693)
 Cogburn, L.A. and Nys, Y.
 Chicken ESTs from reproductive tract
 Unpublished (2002)
 Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers
 1..693
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Commercial broiler and layer"
 /db_xref="taxon:9031"
 /clone="pgrin.pk004.g6"
 /sex="Male and Female"
 /tissue_type="Testis, ovary and oviduct"
 /dev_stage="Various stages; embryonic, post-hatch, immature
 and sexually-mature"
 /lab_host="E. Coli EMDH108"
 /clone_lib="Normalized chicken reproductive tract cdna
 library (pgrin)"
 /note="vector: pCMVSPORT6; Library made from three total
 RNA pools from each tissue (testis 25%, ovary 25%, and
 oviduct 50% of final RNA pool) Single pass sequencing from
 5'-end"

ORIGIN

Query Match 17.9%; Score 179.2; DB 6; Length 693;
 Best Local Similarity 59.4%; Pred. No. 3.2e-37;
 Matches 360; Conservative 0; Mismatches 238; Indels 8; Gaps 3;
 Qy 43 TGCCAGTCTTCAGAGAGTACAGCAAGTCTACTCTCCCTGGCCTACAGTATCATCTTT 102
 Db |||||
 Qy 67 TGCACCTTCCATGAGGAATTCAGCAGGTCTCTGTCGCCCTGGTCTACTCAGTGGTGTTC 126
 Db |||||
 Qy 103 ATCTAGGGCTGCCACTAAATGGCAGTCTCTTGGGCACTTCTCGGGCCAAACCAAGCGC 162
 Db |||||
 Qy 127 CTACTGGGGCTGCCACTCAATGCCGTGTCTATGGCAGATCTGGCTGGCCCGCAAGCGC 186
 Db |||||
 Qy 163 TGGAGCTGTGCGCACCACTATCTGGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTA 222
 Db |||||
 Qy 187 TTGACCCGCAACCACTACATGCTGAACCTGGCCATGGCCGACCTGCTTTATGTCTGC 246
 Db |||||
 Qy 223 T---TGCCCTTCTCATCATCCTACTCATAGATGACAGGTGGCCCTTCGGGGAGCTG 279
 Db |||||
 Qy 247 TCCCTCCCTCTCTCTCATCTACATACACCCAGAGGATTTACTGGCCCTTTGGGGACTTC 306
 Db |||||
 Qy 280 CTCTGCAAGCTGGTGCACTTCTCTTCTATATCAACCTTTACGCGCAGCATCTCTGCTGTG 339
 Db |||||
 Qy 307 ACCTGCAAAATTCGTCGCCGTTCAGTTCTACACCAACCTGCAACGAGCATCTCTTCTCTC 366
 Db |||||
 Qy 340 ACCTGCAATCTCTGTGCAACCACTTCTAGGTGTGTGCGCACCCACCTGCTGTGCTGCTAC 399
 Db |||||
 Qy 367 ACCTGCAATCAGGTCGCGGCTACATGGGATCTGCCACCCCTTTGGCCTCGTGCACAAA 426
 Db |||||
 Qy 400 CGGACCCG---CAGGCATGCTGGCTGGGCAACAGCACCACTGGGCCCTGGTGGTCTCTC 456
 Db |||||
 Qy 427 AAGAGGGAAGAAGCTGACGTGGCTGTGTGTGCTGCGGTGTGCTGCTGCTGCTGCTGCTGCT 486
 Db |||||

QY 457 CAGTGTGTCGCCACACATGGGCTTCTCCACACAGGACTACATCAATGGCCAGATGATCTGG 516
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 Db 487 CAGTGGCTGGCCACCTTGTCTTCCGCTCCACGCGCAGCAGAGAAATCGCACTGTCTGC 546
 |||||
 QY 517 TATGACATGACCGACGACAGAGAAATTTGATCGGCTTTTTCCTACGCGCATAGTCTTGACA 576
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 Db 547 TATGACATGAGCCCCCGGACCGCTCCACATCTTCTTCCCTATGGCATACAGTTGACC 606
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 QY 577 TTGTCTGGCTTTCT--TTCCCTCTTGTGTCAATTTTGTGTGCTATTTCACCTGATGGTCAGG 634
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 Db 607 ATCAGCGGCTTCTGCTGCTGCTTCCGAGCCATCTGCGCTCTACTGCGCATGGCCCGC 666
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 QY 635 AGCCTG 640
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 Db 667 ATCCTG 672
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RESULT 6
 DQ052984
 LOCUS
 DEFINITION Pan troglodytes P2RY2 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION DQ052984
 VERSION DQ052984.1 GI:66898931
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Pan.
 REFERENCE 1. (bases 1 to 1073)
 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
 Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
 White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 A Scan for Positively Selected Genes in the Genomes of Humans and
 Chimpanzees
 (er) Plos Biol. 3 (6), E170 (2005)
 15869325
 REFERENCE 2. (bases 1 to 1073)
 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
 Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
 White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
 Direct Submission
 Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment. Translation starts at the beginning of
 alignment.
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 /db_xref="taxon:9598"
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 <1..>1073
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 /locus_tag="HC13517"
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 Query Match 17.7%; Score 177.2; DB 11; Length 1073;
 Best Local Similarity 42.6%; Pred. No. 1.3e-36;
 Matches 367; Conservative 0; Mismatches 486; Indels 8; Gaps 3;
 QY 43 TGGCAGTTCTCAGAGAAAGTACAAGCAAGTCTTACCTCTCCCTGGCCTACAGTATCATCTTT 102
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 Db 28 TGCNNNTCAACGAGGACNTCAAGTACNNNTCTGCTGCTGTNTCNACGGGTGTGTGT 87
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 QY 103 ATCTAGGGTGGCCACTAAATGGCACTGTCTTGGGCACCTTCTGGGCGCAACCAAGCGC 162
 |||||
 Db 88 GTGCTGGGCTGTGNNNGAAGCGCGTGCNNNNNCAANNNTCNTGTNNNNNCAAGANC 147
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 QY 163 TGGAGCTGTGCCACCACTATCTCTGGTGAACCTGATGTTGGCGCACTCTTATGTGCTA 222
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Db 148 TGGAAATGNTCNNNNNATATATGTTNNNCTGGTGTCTGTGATGCACATGTATGCGGCC 207
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 QY 223 T---TGCCCTTCTCATATCATATCACTACTCATAGATGACAGGTGGCCCTTTGGGGAGCTG 279
 |||||
 Db 208 TCCCTGCGGTGTGTGTCTATTACTACGCCGCGGGACCACTGGGCCCTTCAGCACGGTG 267
 |||||
 QY 280 CTCTGCAAGTGTGTGCACTTCTCTTATATCAACTTTACGCGAGCATCTGCTGCTG 339
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 Db 268 CTCTGCAAGTGTGTGCGCTTCTCTTACCAACCTTTTACTGCAAGCATCTTCTTCCCTC 327
 |||||
 QY 340 ACCTGATCTCTGTGACCAAGTTCCTTAGGTGTGTGCGCACCACTGTGTTCGCTGCCCTAC 399
 |||||
 Db 328 ACCTGATCAGCGTGCACCGTGTCTGGGGTCTTAGGACCTCTGCGTCCCTCGCGTGG 387
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 QY 400 CGGACCCGCGAGGATGCTGGTGGGCAACAGCAACCACTGGGCCCTCTGGTGGTCTCTCCAG 459
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 Db 388 GCGCGGCGCGCTACGCTGCGCGGTGGCGCGGCGCTGTGGTGTGGTGGCGCTGC 447
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 QY 460 CTGCTGCCACACATGGGCTTCTCCACACGGACTACATCAATGGCCAGATGTGTAT 519
 |||||
 Db 448 CAGGCCCCCGTGCNNNACTTTGTNNNNCAGCGCGCGGGGCGCGNNNTAACTGCGCAC 507
 |||||
 QY 520 GACATGACCAAGCAAGAGAAATTTGATCGGCTTTTGGCCTACGGCATAGTCTTGACATTG 579
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 Db 508 NACACNNNGNACCCGACGNNNTCAGCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNN 567
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 Db 568 NNN 627
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 QY 638 CTGATCAAGCCAGGAGGAACTCATGAGGACAGGCAACACAGCCCGAGCGCATC 697
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 Db 628 CTCTAAAGCCNN 687
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 QY 698 CGGACCATCTACTGTGTGTGGCTCTTCAACCCTCTGTTTGTGGCCTTCCATATCACT 757
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 Db 688 NNN 747
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 QY 758 CGCTCTTCTTACCTCACCATCTGCTTCTTGTCTTCTCAGGACTGCGCAGCTCTTGTATGGCA 817
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 QY 818 GCCAGTGTGGCTTACAGATATGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCCTCAACCCA 877
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 Db 805 ATCAACATGGCCCTACAAGGTTACCCGCGCTGCGCAGTCTAACAGTTGCGCTTGACCCC 864
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 QY 878 GTCTGTACTTTCTTTCAAGG 898
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 Db 865 GTGCTTACTTCTGGCTGG 885
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RESULT 7
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 DEFINITION Homo sapiens P2RY6 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY400797
 VERSION AY400797.1 GI:39756786
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1. (bases 1 to 987)
 Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL
 PUBMED 14671302

[illegible]

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QY 279 GCTCTGCAAGCTGGTGCACCTTCCTGTTCTATATCAACCTTTACGGCAGCATCCTGCTGCT 338
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464 CGCTGCGCGCTGGTGCCTGCTCTCTTCTATGCAACCTTCACGGCAGCATCCTCTTCCT 523
QY 339 GACCTGATCTCTGTGCACAGTTCCTAGGTGTGTGCGCACCCACTGTGTTCGCTGCCCTA 398
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
524 CACCTGATCAGTTCCTCAGGGCTACCTTGGGCACTGCGACCCGCTGGCCCCCTGGACAA 583
QY 399 CC---GGACCGCAGGATGCTGGCTGGGACACAGACCACTGGGCCCTGTGTGTCCT 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
584 ACGTGGGGCGCGCGGCTGCTGGCTAGTGTGTGTAGCGGTGTGTGGCTGGCGGTGACAAC 643
QY 456 CCAGCTGCTGCCACACTGGCTTCTCCACAGGACTATCAATGGCCAGATGATCTG 515
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
644 CCACTGCTGCCACAGCCATCTTCCTGTGCGCACAGGATCCAGCGTAACCGCACTGTCTG 703
QY 516 GTATGACATACACAGCAAGAAATTTTGATCGGCTTTTGGCTTACGGCATAGTTCGTAC 575
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
704 CTATGACTCAGCCCGCTGCCCTGGCCACCACTATATGCCCTATGCGATGGCTCTCAC 763
QY 576 ATTGTCTGGCTTCT--TTCCCTCTTGGTCAATTTTGGTGTCTATTCTGATGTCAG 633
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
764 TGTATCGCTTCTGCTGCGCTTGTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 823
QY 634 GAGCTGATCAAGCCAGGAGAACCTCATGAGGACAGGCAACACAGCCGAGCCAGGTC 693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
824 CCGCTTGTGCGCAGGATGGCCGCGAGACCTGTGGCCACAGGCGGCTGGCAAGGC 883
QY 694 CATCGGACCATCTACTGTGTGTGCGCTTTCACCTCTGTTTGTGCGCTTCCATAT 753
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884 GGCCCGATGGCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
QY 754 CACTCGTCTTCTACCTACCACTGCTCTTCTGCTTCTCAGGACTGCCAGCTCTTGAT 813
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
944 CACCAAGACAGCTTACTGGCAGTGCCTGACGCGCGGCTGCCCTGCACTGTATTGGA 1003
QY 814 GGCAGCAGTGTGCGCTACAGATATGAGGCTCTGCTGAGTGTGAGAGCTGCTCCTCAA 873
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1004 GGCCTTTGCAAGCGCTTACAAAGCACGCGCGCTTTGGCAGTGCCAAACAGCGTGTGA 1063
QY 874 CCCAGTCTGTACT 887
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1064 CCCATCTCTTCT 1077
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```
RESULT 9
CR612681 1515 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI044YA15 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR612681
VERSION CR612681.1 GI:50493488
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1515)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1515)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
```

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source

1. .1515

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI044YA15"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

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Query Match 16.4%; Score 164.8; DB 4; Length 1515;
Best Local Similarity 52.0%; Pred. No. 3.3e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

QY 42 CTGCCAGTTCTCAGAGAGTACAAAGTCTACCTCTCCCTGCGCTACAGTATCATCTT 101
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
312 CTGTGCTACCGGAGAACTTCAAGCAACTGTGCTGCCACCTGTGTATTTCGGGGTGCT 371
QY 102 TATCTAGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGGCCAAACCAAGCG 161
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
372 GCGGCTGGCTGCCGTGAACATCTGTGTATTACCCAGATCTGCACGTCGCCGCGGC 431
QY 162 CTGGAGTGTGCCACACCACTATCTGTGTAACTGTATGGTGGCGCACTGTCTTATGTGCT 221
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
432 CTTGACCCGACGCGCGGTGTACACCCCTAAACCTTGTCTGGCTGACCTGTATATGCTG 491
QY 222 AT---TGCCCTTCTCATCATCACTACTACATAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
492 CTCCTTGGCCCTGCTCATCTACAACATATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 551
QY 279 GCTCTGCAAGCTGGTGCACCTTCTGTTTATATCAACCTTTACGGCAGCATCTCTGTGCT 338
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
552 CGCTTGGCGCTGGTTCGCTTCTCTTATGCAACCTGCACGCGAGCATCTCTTCTCT 611
QY 339 GACTGTGATCTGTGTGACCAAGTTCCTAGTGTGTGCGACCCCACTGTGTTCGCTGCCCTA 398
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
612 CACTGTGATCAGCTTCAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCCCTGGCACAA 671
QY 399 CC---GGACCCGAGGATGCTGGCTGGGACACAGCACCTGCGCCCTGTGTGCTCT 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
672 ACGTGGGGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
QY 456 CCAGCTGCTGCCACACACTGGCTTCTCCCAACGAGTATCATCAATGGCCAGATGATCTG 515
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
732 CCAGTGGCTGCCACAGCCATCTTCGTCGCACAGGATCCAGCGTAACCGCACTGTCTG 791
QY 516 GTATGATGACAGCAGCCAGAGAAATTTTGTATCGGCTTTTGGCTTACGGCATAGTTCGAC 575
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
792 CTATGACCTCAGCCCGCTGCCCTGGCCACCCACTATATGCCCTATGCGCATGGCTCTCAC 851
QY 576 ATTGTCTGGCTTCT--TTCCCTTCTGCTGTCATTTTGGTGTGCTATTCTGATGTGTCAG 633
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
852 TGTATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
QY 634 GAGCTCTGATCAAGCCAGAGAGAACTCTATGAGGACAGGCAACACAGCCCGAGCAGGTC 693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
912 CCGCTTGTGGCGCAGGATGGCCCGGAGAGCCCTGTGGCCAGGAGCGGCTGGCAAGGC 971
QY 694 CATCCGAGCATCTTACTGTGTGTGGCTCTTTCACCCCTCTGTTTGTGGCTTCCATAT 753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
972 GGCCTCGCATGGCGTGTGTGTGCTGTGCTTTTGGCCATCAGCTTCTGCTCTTTTCAT 1031
QY 754 CACTCGCTCTTCTACTACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 813
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1032 CACCAAGACAGCCTTACTTGGCAGTGGCTCGACCGGGCGTCCCTCTGCACTGTATTGGA 1091
QY 814 GGCAGCCAGTGTGGCTTACAAAGATATGGAGGCTCTGCTGGTGTGTGTGAGCAGCTGCCTCAA 873
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1092 GGCCTTTGACGCGCTTACAAAGGACGCGCGCGCTTTGGCCAGTGTGCCAACAGCGGTGGA 1151
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Qy 874 CCCAGTCTCTACT 887
    ||| ||| |||
Db 1152 CCCATCTCTTCT 1165

RESULT 10
CR618945 1532 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI042YA16 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR618945
VERSION CR618945.1 GI:50499752
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1 (bases 1 to 1532)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
REFERENCE 2 (bases 1 to 1532)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefegenoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES             Location/Qualifiers
     source            1..1532
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
                        /db_xref="taxon:9606"
                        /clone="CSODI042YA16"
                        /tissue type="Placenta Cot 25-normalized"
                        /plasmid="pCMVSPORT_6"

ORIGIN
Query Match      16.4%; Score 164.8; DB 4; Length 1532;
Best Local Similarity 52.0%; Pred. No. 3.3e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

Qy 42 CTGCAGTTCTCAGAGAGTACAGCAAGTCTACTCTCTCCCTGGCCTACAGTATCATCTT 101
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 CTGTGTCTACCGCGAGAACTTCAAGCAACTGCTGCTGCCACCTGTGTATTCCGGCGGTGCT 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 102 TATCTAGGGTGCACCTAAATGGCACCTGCTTGTGGCACTTCTGGGCGCCAAACCAAGCG 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 372 GCGGCTGGCTGGCGCTGAACATCTGTGTATACCAGATCTGCAGTCCCGCGGCG 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 162 CTGGAGCTGTGCCACCACTATCTGGTGAACCTGATGGTGGCGGACCTGCTTTATGTGCT 221
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 CTTGACCGCGACGCGGTGACACCTAAACCTTGTCTGTGGCTGACCTGTATATGCTG 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 222 AT---TGGCCTTCCTCATCATCACTACTCTAGATGACAGGTGGCCCTTCGGGGAGCT 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 492 CTCCTGGCCCTGCTCATCACTCAACTATGCCCAAGGTGATCACTGGCCCTTTGGCGACTT 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 279 GCTCTGCAAGCTGGTGCATCTTCTCTTATATCAACTTTACGCGACATCCTGCTGCT 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 552 GCGCTGGCGCTGGTGGCGCTTCTCTTATATGCAACTTGCACGCGACATCTCTTCTCT 611
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Qy 339 GACCTGCATCTCTGTGCACCAAGTTCCTAGGTGTGTGCCACCACTGTGTTCGCTGCCCTA 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 CACCTGCATCAGCTTCCAGCGCTACTCTGGGCATCTGCCACCGCTGCGCCCTCGSCAA 671
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Qy 399 CC---GGACCGCAGGCATGCTGCTGGGCGCACCGACACACCTGGGCGCTGGTGCTCT 455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 672 ACGTGGGGGCGCGCGGCTGCTGGCTAGTGTGTAGCGGTGGTGGCGGTGACAAAC 731
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 456 CCAGCTGTGCTGCCACACTGGGCTTCTCCACACAGGACTACATCAATGATGATGATCTG 515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 732 CCAGTGTGCTGCCACAGCCATCTTGGCTGCGCACAGGATCCAGCGTAACCGCACTGTCTG 791
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 516 GTATGACATGACCAAGCAAGATTTTGTATGCGCTTTTGGCTTACGGCATAGTCTGAC 575
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 792 CTATGACCTCAGCCCGCTGCTGGCGACCCACTATATGCCCTATGCGCATGGCTCTCAC 851
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 576 ATTGTCTGGCTTCTCT---TTCCTCTCTTGGTCAATTTGGTGTGCTATTCACTGATGGTCTG 633
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 852 TGTATCATGGCTTCTGCTGCGCTTGTGCGCTGCTGCGCTGCTACTGTCTCTGGGCTG 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 634 GAGCTGATCAAGCCAGAGGAGAACTCATGAGACAGGCAACACAGCCCGAGCCAGGTC 693
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 912 CCGCTGTGCGCGCAGGATGGCCGCGAGAGCCTGTGGCCAGGAGCGCGTGGCAAGGC 971
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 694 CATCGGACCATCTACTGCTGTGGCTTTCACCTCTGTTTGTGGCCCTTCCATAT 753
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 972 GCGCCGATGCGCTGTGTGGCTGTGCTTGTGCCATCAGCTTCTCTGCTTTTCAT 1031
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 754 CACTCGCTCTTCTACCTCACCATCTGCTTCTCTTCTCAGGACTGCCAGCTCTTGAT 813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1032 CACCAAGACACCTACTCTGGCAGTGCCTCGACGCCGGCGCTCCCTGCACTGATTGGA 1091
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Qy 814 GGCAGCCAGTGTGGCTTACAGATATAGAGGCTCTCTGGTGTGTGAGCAGCTGCCCAA 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1092 GGCCTTTTGACGCGGCTTACAAAGGACACGCGGCCCTTTGCCAGTGCCAAACGCGTCTGA 1151
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 874 CCCAGTCTCTACT 887
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1152 CCCATCTCTTCT 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
CR626266 1564 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI038YC15 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR626266
VERSION CR626266.1 GI:50507073
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominidae; Homo.
REFERENCE 1 (bases 1 to 1564)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
REFERENCE 2 (bases 1 to 1564)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefegenoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES             Location/Qualifiers
     source            1..1564
                        /organism="Homo sapiens"
                        /mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="CS0D1024YE14"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="PCMVSPORT_6"

ORIGIN
Query Match      16.4%; Score 164.8; DB 4; Length 1564;
Best Local Similarity 52.0%; Pred. No. 3.3e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

QY 42 CTGCGAGTCTTCAGAGAGTACAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTT 101
   |||
Db 343 CTGTGTCTACCGGAGAACTTCAAGCAACTGCTGCTGCCACCTGTGTATTTCGGGGTCT 402
   |||

QY 102 TATCTTAGGCTGCCATAAATGGCACTGTCTTGTGGCACTTCTTGGGGCCAAACCAAGCG 161
   |||
Db 403 GCGGCTGGCTGCGCTGCAACATCTGTGTCAITACCCAGATCTGCACGTCCCGCCGGC 462

QY 162 CTGGAGCTGTGCCACCACTCTCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTCT 221
   |||
Db 463 CTTGACCCGACGCGCTGTGTACACCTTAAACCTTGTCTTGGCTGACCTGTATATGCTG 522

QY 222 AT---TGCCCTTCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
   |||
Db 523 CTCCCTGCGCTGTCTATCTACACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 582

QY 279 GCTCTGAAGCTGTGCATCTCTCTTCTATATCAACCTTTTACGGCAGCATCTCTGTCT 338
   |||
Db 583 CGCTGTGCGCTGTGCTGCTTCTTCTATATGCAACCTGTGCAACCTGTGCAACCTCTCTTCT 642

QY 339 GACTGTGATCTGTGTGACCACTTCTAGTGTGTCACCACTGTTGTGGTGGCCCTA 398
   |||
Db 643 CACTGTGATGACTTTCAGGCTTACCTGAGGATCTGCAACCTGCGCTGGCCCTGGCACAA 702

QY 399 CC---GGACCCGACGAGCATGCTGGCTGGGCGACAGCACCACCTGGGCGCTGTGTGCT 455
   |||
Db 703 ACGTGGGGCGCGCGCTGCTGCTGTGTGTAGCGGTGTGGCTGGCGGTGACAA 762

QY 456 CCAAGCTGTGCGCCACACTGGCTTCTCCACAGCACTATCAATGGCCAGATGATCTG 515
   |||
Db 763 CCAAGTGTGCGCCACAGCATCTTCTGCTGCGCAGGATCCAGCGTAAACCGCACTGTCTG 822

QY 516 GTATGATGATGACCAAGCAAGAGATTTTGTATCGGCTTTTGGCTTACGGCATGTTCTGAC 575
   |||
Db 823 CTATGACCTCAGCCCGCTGCTGCTGCGCACCCACTATATGCCCTTATGGCATGCTCTCAC 882

QY 576 ATTGCTGTGGCTTCT--TTCCCTCTTGTGTCATTTTGTGTGCTATTTCACTGATGCTGAG 633
   |||
Db 883 TGTATCGGCTTCTGTGCTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942

QY 634 GAGCTGATCAAGCCAGGAGAACCTCTATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
   |||
Db 943 CCGCTGTGCGCGCAGGATGGCCCGCAGAGCCTGTGGCCAGAGCGGGGTGGCAAGGC 1002

QY 694 CATCCGAGCATCTACTGTGTGTGCGCTTTCACCTCTGTGTGTGCTGCTTCCATAT 753
   |||
Db 1003 GCGCCGATGGCCGTGTGTGTGCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1062

QY 754 CACTGCTCTCTTACCTCACCATCTGCTTCTCTCTTCTCAGGACTGCCAGCTCTTGAT 813
   |||
Db 1063 CACCAAGACAGCTTACTTGGCAGTGGCTCGAGCGCGGGCGTCCCTTGCACTGATTTGA 1122

QY 814 GGCAGCAGTGTGCGCTTCAAGATATAGAGCCCTCTGTGTGTGTGTGTGTGTGTGTGTGT 873
   |||
Db 1123 GGCCTTTGACGCGCTTCAAAAGGACGCGCGCTTTGCGAGTGCACCAACAGCGTGTGGA 1182

QY 874 CCAAGTCTGTACT 887
   |||
Db 1183 CCCATCTCTTCT 1196

RESULT 12
CR626754
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Best Local Similarity 52.0%; Pred. No. 3.3e-33; Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;	
Qy	42 CTGCCAGTTCTCAGAGAAAGTACAAGCAAGTCTACCTCTCCCTGGCTCTACAGTATCATCTT 101
Db	390 CTGTGTCTACCGGAGAACTTCAAGCAACTGCTGCTGCCACCTGTGTATTTCGGCGGTGCT 449
Qy	102 TATCTTAGGGCTGCCACTAAATGGCACTGTCCTTTGGGCACTTCTGGGGCCAAACCAAGCG 161
Db	450 GGGGGTGGGCTCGCGTGAACATCTGTGTCAATTAACCCAGATGCAACGCTCCCGCGGGC 509
Qy	162 CTGGAGCTGGCCACCAACCTATCTGCTGAACTGATGTTGGCCGACCTGCTTTATGTGCT 221
Db	510 CCTGACCCGACGGCGGTGTACACCTTAAACCTTGTCTTGGCTGACCTGCTATATGCTG 569
Qy	222 AT---TGCCCTTCTCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTTCGGGAGCT 278
Db	570 CTCCTTGCCCTGCTCATCTACAACTATGCCAAAGTGATCACTGGCCCTTTGGGACATT 629
Qy	279 GCTCTGAAGCTGGTGCACTTCTCTGTATTATCAACCTTTAGCGGAGCATCTCTGTGCT 338
Db	630 CGCTGCTCGGCTTGGTCCGCTTCTCTTATGCAACCTTGCACGGGAGCATCTCTTTCCT 689
Qy	339 GACTGATCTCTGTGCACCACTTCTAGGTGTGCAACCACTGTGTTCGTGCTGCCCTA 398
Db	690 CACTGTGATCAGCTTCCAGCGCTACCTTGGGCATCTGCCACCCCTGGCCCTTGGACAA 749
Qy	399 CC---GGACCCGAGGCATGCTTGGCTGGGCACACGACCACTTGGGCCCTTGGTGTCT 455
Db	750 ACGTGGGGCGCGGGCTGCTGTGTGTGTAGCGGTGTGGCTGGCCCTGACAA 809
Qy	456 CAGCTGCTGCCACACTGGCCCTTCTCCACAGGATACATCAATCAATGGCCAGATGATCTG 515
Db	810 CCAAGTGTCTCCACAGCCATCTTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTG 869
Qy	516 GTATGATCATCACAGCAAGAGAAATTTTGATCGCTTTTGGCTTACGGCATAGTTCGTGAC 575
Db	870 CTATGACCTCAGCCCGCTGCTTGGCCACCACTATATGCCCTATGGCATGGCTCTCAC 929
Qy	576 ATTGTCTGGCTTCT--TTCCCTCTTGTGTCATTTTGGTGTGCTATTTCATGTAGTGTGAC 633
Db	930 TGTCTATCGGCTTCTGCTGCCCCCTTGTGCTGCTTGGCTGCTACTGTCTCTGGCCTG 989
Qy	634 GAGCTGTATCAAGCCAGAGAGAACTCTATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
Db	990 CCGCTGTGCGCGCAGGATGGCCCGGACAGGCTGTGGCCAGGAGCGGCTGGCAAGGC 1049
Qy	694 CATCCGGACCATCTCTACTGTGTGTGGCTCTTCACTGCTTGTGCTTGTGGCTTCCATAT 753
Db	1050 GGCCCGCATGGCGTGGTGTGCTGCTGCTTGGCATGAGTCTCTGCTTTTTCAT 1109
Qy	754 CACTGCTCTTCTTACTCTACCATCTGCTTCTTGTCTTCTTCTCAGACTGCGAGCTCTTGAT 813
Db	1110 CACCAAGACAGCTTACCTGGCAGTGGCTCGACGCGCGGGCTGCCCTGCACTGTATTGGA 1169
Qy	814 GCGAGCCAGTGTGGCTTACAGATATGGAGGCTCTGTCAGTGTGAGCAGCTGCCTCAA 873
Db	1170 GGCTTTTTCAGCGGCTTACAAAGGCAACGCGGCGCTTTGGCAGTGCCAAACGCTGCTGGA 1229
Qy	874 CCCAGTCTCTTACT 887
Db	1230 CCCATCTCTTCT 1243
RESULT 14	
LOCUS	CR606834
DEFINITION	full-length cDNA clone CS0DC014YB07 of Neuroblastoma Cot 25-normalized of Homo sapiens (human) .
ACCESSION	CR606834
VERSION	CR606834.1 GI:50487641
KEYWORDS	HTC; CNSLT cDNA.
SOURCE	Homo sapiens (human)


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Qy 102 TATCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 475 GCGGCTGGCGTGGCGTGAACATCTGTGTATTACCCAGATCTGCAGTCCCGCGGGC 534
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 162 CTGGAGCTGTGCCACCACTATCTGGTGAACTGTATGTGGCGGACCTGCTTTATGTGCT 221
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 535 COTGACCCGCGAGGCGGTACACCTAAACCTTGTCTGTGGCTGACCTGCTATATGCGCTG 594
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 222 AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 595 CTCCCTGCCCCTGCTCATCTCAACTATGCCCAAGGTGATCACTGGCCCTTTGGGACTT 654
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 279 GCTCTGAAGCTGTGCACTTCTCTCTTATATCAACCTTTACGGCAGCATCTGCTGCT 338
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 655 CGCCTGCGCGTGGTTCCTTCTTATGCCAACTTGCAOGGCAGCATCTTCTTCT 714
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 339 GACCTGCATCTCTGTGACCACTTCTAGGTGTGTGCCACCGCATGTGTTCGCTGCCCTA 398
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 715 CACCTGCATCAGCTTCCAGCGCTACTGGGCATCTGCCACCGCTGGCCCTGGCACA 774
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 399 CC---GGACCCGCGAGCATGCTGGCTGGCCACAGCACCTGGGGCCCTGGTGGTCT 455
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 775 ACGTGGGGCGCGCGGCTGCTGCTAGTGTGTAGCGGTGTGGCTGGCCGTGACAAC 834
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 456 CCAGCTGCTGCCACACTGGGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG 515
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 835 CCAGTGCCTGCCACAGCATCTTCGCTGCCACAGGCATCCAGCGTAACCGCATGTCTG 894
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 516 GTATGACATGACCGCAGAGAAATTTTGTATGCGGCTTTTTCCTACGGCATAGTTCTGAC 575
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 895 CTATGACCTCAGCCCGCTGCGCTGGCCACCCACTATATGCGCTATGGCATGGCTCTCAC 954
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 576 ATTGTCTGGCTTCT--TTCCCTCTTGGTCACTTTTGGTGTGCTATTCACTGATGGTCA 633
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 955 TGTCACTGGCTTCTGCTGCGCTTGTGCGCTGCTGCGCTGCTGCTGCTGCTGCTGCTG 1014
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 634 GAGCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1015 CCGCTGTGCGCCAGGATGGCCCGGAGAGCCTGTGCCCCAGGAGCGGCGTGGCAAGC 1074
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 694 CATCCGGAACATCTACTGCTGTGTGTGCGCTCTTCACTCTGTGTGTGTGTGTGTGTGT 753
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1075 GCGCCGATGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1134
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 754 CACTCGCTCTTCTACTCACTCACTCTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 813
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1135 CACCAAGACAGCCTACCTGGCAGTGCCTCGACGCGCGGCGTCCCTGCACTGTATTGGA 1194
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 814 GGCAGCCAGTGTGGCTTACAAGATATGAGGCGCTCTGGTGTGTGTGTGTGTGTGTGTGT 873
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1195 GGCCTTTGCAGGGGCTTACAAGGACGCGGCGGCTTGGCCAGTGCACAGGCTGCTGGA 1254
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 874 CCCAGTCTCTACT 887
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1255 CCCCATCCTCTCT 1268
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Job time : 4767 secs

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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 10:33:06 ; Search time 647 Seconds
(without alignments)
10321.518 Million cell updates/sec

Title: US-10-088-726-25
Perfect score: 1002
Sequence: 1 atgaggaaggtggacatgaa.....ggttgaacagatctgggtaa 1002

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_21.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002as.*
- 7: geneseqn2002bs.*
- 8: geneseqn2003as.*
- 9: geneseqn2003bs.*
- 10: geneseqn2003cs.*
- 11: geneseqn2003ds.*
- 12: geneseqn2004as.*
- 13: geneseqn2004bs.*
- 14: geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1002	100.0	1002	4	Aah73516 Human G p
2	1000.4	99.8	1156	10	Adb99267 Human p2Y
3	1000.4	99.8	1334	10	Adc86166 Human GPC
4	1000.4	99.8	3143	6	Aas17746 Human gen
5	996.4	99.4	1082	6	Abq76000 Human GPC
6	983.4	98.1	1063	6	Aas98135 Human DNA
7	977.4	97.5	1108	6	Adi16629 Human NOV
8	977.4	97.5	1108	12	Adn42283 Human CDN
9	920.4	91.9	1017	10	Adc25999 Human pur
10	920.4	91.9	1017	10	Aad61648 Human GPC
11	917.2	91.5	1020	6	Abq79300 Human GPC
12	917.2	91.5	1076	6	Aad29667 Human G-p
13	917.2	91.5	1076	12	Ado30395 Human GPC
14	848.4	84.7	850	6	Aas17747 Human p2Y
15	604.6	60.3	906	12	Ado30397 Mouse GPC
16	510	50.9	510	6	Aah50975 Human nGP
17	510	50.9	510	6	AbS70208 DNA encod
18	400.4	40.0	681	4	Aas30774 Human CDN
19	374	37.3	585	4	Aas30783 Human CDN

20	237.4	23.7	1163	12	ADP49190	Adp49190 Chick p2Y
21	229.4	22.9	1134	12	ADO30017	Ado30017 Human GPC
22	229.4	22.9	2025	4	AAO04980	Aao04980 Human pur
23	229.4	22.9	2025	6	ABZ35611	Abz35611 Human gen
24	229.4	22.9	2025	8	ABZ42713	Abz42713 Human pur
25	229.4	22.9	2025	10	ACA56884	Aca56884 Human sig
26	229.4	22.9	2025	12	ADI56680	Adi56680 Human pol
27	229.4	22.9	2025	12	ADP49188	Adp49188 Human p2Y
28	227.8	22.7	2118	6	ABZ35320	Abz35320 Human gen
29	226.2	22.6	2547	12	ADP21380	Adp21380 Gene p2RY
30	225.2	22.5	1163	4	AAO04981	Aao04981 Human pur
31	203.8	20.3	1122	12	ADO30307	Ado30307 Mouse GPC
32	203.8	20.3	1842	2	AAQ88134	Aaq88134 Human p2O
33	203.8	20.3	2138	6	AAO32944	Aao32944 Mus muscu
34	203.8	20.3	2138	6	AAO32937	Aao32937 Mus muscu
35	189.4	18.9	2011	10	ADB52840	Adb52840 Primary r
36	189.4	18.9	2011	13	ADV41117	Adv41117 Rat cardi
37	180.2	18.0	1098	8	ABZ42771	Abz42771 Human pyr
38	180.2	18.0	1098	12	ADO30018	Ado30018 Human GPC
39	180.2	18.0	1428	12	ADP21381	Adp21381 Gene p2RY
40	180.2	18.0	1429	2	AAO74321	Aao74321 Human p2Y
41	180.2	18.0	1429	10	ACA56470	Aca56470 Human sig
42	180.2	18.0	1429	12	ADI56266	Adi56266 Human pol
43	180.2	18.0	1429	12	ADP49192	Adp49192 Human p2Y
44	175.4	17.5	1651	10	ADE40462	Ade40462 Human pyr
45	170	17.0	234	4	AAS30782	Aas30782 Human CDN

ALIGNMENTS

RESULT 1

AAH73516

ID AAH73516 standard; DNA; 1002 BP.

XX AC AAH73516;

DT 25-SEP-2001 (first entry)

DE Human G protein-coupled receptor GPRV71 coding sequence.

XX Human; guanosine triphosphate binding protein-coupled receptor;

KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;

KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;

KW Alzheimer's disease; cytostatic; hepatotropic; neurotropic;

KW neuroprotective; gene therapy; peptide therapy; db.

XX Homo sapiens.

XX WO200148188-A1.

PN 05-JUL-2001.

PD 28-DEC-2000; 2000WO-JP009408.

PF 28-DEC-1999; 99JP-00375152.

PR 31-MAR-2000; 2000JP-00101339.

XX (HELI-) HELIX RES INST.

PA Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;

PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;

PI WPI; 2001-425662/45.

XX P-PSDB; AAG64125.

XX New DNA encoding guanosine triphosphate binding protein coupled receptors

PT and their expression products for screening potential anticancer and

PT neurotropic drugs and in diagnosis of these diseases.

XX Example 1; Page 142-143; 170pp; Japanese.

XX The invention relates to nine human guanosine triphosphate binding

CC

CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,
CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
CC present sequence is a G protein-coupled receptor coding sequence of the
CC invention
XX
SQ Sequence 1002 BP; 207 A; 293 C; 249 G; 253 T; 0 U; 0 Other;
Query Match 100.0%; Score 1002; DB 4; Length 1002;
Best Local Similarity 100.0%; Pred. No. 7.4e-263;
Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAGAGAGGTGGACATGATATACATACAGGAAACAGAGTCTCTGCCCAATGTTCTCAGAGAAG 60
Db 1 ATGAGAGAGGTGGACATGATATACATACAGGAAACAGAGTCTCTGCCCAATGTTCTCAGAGAAG 60
Qy 61 TACAAGCAAGTCTACCTCTCGCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 61 TACAAGCAAGTCTACCTCTCGCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Qy 121 AATGGCACTGTCTTGTGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180
Db 121 AATGGCACTGTCTTGTGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180
Qy 181 TATCTGGTGAACCTGTATGGTGGCCGACCTGCTTTATGTGTATTTATGCTTATGCTTCTCATCATC 240
Db 181 TATCTGGTGAACCTGTATGGTGGCCGACCTGCTTTATGTGTATTTATGCTTATGCTTCTCATCATC 240
Qy 241 ACCTACTCATAGATGACAGTGGCCCTTGGGAGCTGTCTGCAAGCTGGTGCACTTC 300
Db 241 ACCTACTCATAGATGACAGTGGCCCTTGGGAGCTGTCTGCAAGCTGGTGCACTTC 300
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCTCATCTCTGTGCCACAG 360
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCTCATCTCTGTGCCACAG 360
Qy 361 TTCTTAGGTGTGTGCCACCACTGTGTTGCTGCTGCCCTACCGGACCCGAGGCAATGCTCGG 420
Db 361 TTCTTAGGTGTGTGCCACCACTGTGTTGCTGCTGCCCTACCGGACCCGAGGCAATGCTCGG 420
Qy 421 CTGGGCAACGACCACTGCGGCCCTGTGGTGTCTCCAGTGTCTGCCCACTGGCCCTTC 480
Db 421 CTGGGCAACGACCACTGCGGCCCTGTGGTGTCTCCAGTGTCTGCCCACTGGCCCTTC 480
Qy 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGTTATGACATGACAGCCAGCAAGAAAT 540
Db 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGTTATGACATGACAGCCAGCAAGAAAT 540
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCCTT 600
Db 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCCTT 600
Qy 601 GGTCAATTTGGTGTGCTATTCTAGTGTGTCAGAGCCTGATCAAGCAGGAGAACT 660
Db 601 GGTCAATTTGGTGTGCTATTCTAGTGTGTCAGAGCCTGATCAAGCAGGAGAACT 660
Qy 661 CATGAGACAGGCAACACAGCCGAGCAGGTCCATCCGACCACTCTACTGGTGTGTGG 720
Db 661 CATGAGACAGGCAACACAGCCGAGCAGGTCCATCCGACCACTCTACTGGTGTGTGG 720
Qy 721 CCTCTTCAACCTCTGTTTTGTGGCCCTTCCATATCACTCGCTCTCTTACCTCAACATCTG 780
Db 721 CCTCTTCAACCTCTGTTTTGTGGCCCTTCCATATCACTCGCTCTCTTACCTCAACATCTG 780
Qy 781 CTTTCTGCTTCTCAGAGCTGCACTCTTGTATGGGAGCCAGTGTGGCTTACAGATATG 840
Db 781 CTTTCTGCTTCTCAGAGCTGCACTCTTGTATGGGAGCCAGTGTGGCTTACAGATATG 840
Qy 841 GAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTCTTTCAAGGGG 900
Db 841 GAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTCTTTCAAGGGG 900

Db 841 GAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTCTTTCAAGGGG 900
Qy 901 GGCAAAAATAGAGTCAAGGCTCTCCAGAAACTGAGGAGAAACAAGTTGGGTGAGCATCCA 960
Db 901 GGCAAAAATAGAGTCAAGGCTCTCCAGAAACTGAGGAGAAACAAGTTGGGTGAGCATCCA 960
Qy 961 GCTGGGAGGAGAGATGCCAGGTTTGAACAGATCTGGGTAA 1002
Db 961 GCTGGGAGGAGAGATGCCAGGTTTGAACAGATCTGGGTAA 1002
RESULT 2
ADB99267
ID ADB99267 standard; cDNA; 1156 BP.
XX
AC ADB99267;
XX AC (first entry)
DT 04-DEC-2003
XX Human p2Y2li cDNA.
DE
XX ss; gene; human; P2Y2li; chromosome 3; G protein-coupled receptor; GPCR;
KW Class A rhodopsin-like sub-family; gene therapy.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 21..1106
FT /*tag= a
FT /product= "P2Y2li"
XX
PN DE10144044-Al.
XX
PD 27-MAR-2003.
XX
PF 07-SEP-2001; 2001DE-01044044.
XX
PR 07-SEP-2001; 2001DE-01044044.
XX
PA (BRUE/) BRUES M.
PA (BOEN/) BOENISCH H.
PA (VKUE/) VON KUEGELGEN I.
XX
PI Brues M, Boenisch H, Von Kuegelgen I;
XX
DR WPI; 2003-364675/35.
DR P-PSDB; ADB99264.
XX
PT New human gene P2Y2li and encoded G protein-coupled receptor, useful for
PT treatment and diagnosis of receptor-associated diseases and for drug
PT screening.
XX
PS Disclosure; Page 4; 6pp; German.
XX
CC This invention describes the human P2Y2li gene and its 5'- and 3'-
CC untranslated regions, located on chromosome 3 which is a novel G protein-
CC coupled receptor (GPCR). The protein encoded by P2Y2li is expressed in
CC blood cells, testis and embryonal kidney cells and contains potential
CC sites for phosphorylation by protein kinase C and casein kinase II. It is
CC a member of the Class A rhodopsin-like sub-family of G protein-coupled
CC receptors and it probably a nucleoside/nucleotide receptor that mediates
CC action of nucleosides/nucleotides or their sugar derivatives. P2Y2li and
CC antibodies directed against the encoded protein are useful in diagnosis
CC and treatment (including gene therapy) of diseases associated with
CC abnormal levels of P2Y2li expression, in screening assays for modulators,
CC potential therapeutic agents, and to produce transgenic animals, e.g. for
CC identifying diseases associated with abnormal expression of P2Y2li. This
CC sequence represents the P2Y2li gene described in the disclosure of the
CC invention.
XX
SQ Sequence 1156 BP; 243 A; 335 C; 295 G; 283 T; 0 U; 0 Other;
Query Match 99.8%; Score 1000.4; DB 10; Length 1156;

Best Local Similarity 99.9%; Pred. No. 2.2e-262;									
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	ATGGAGAGGTGGACATGAATACATACAGGACAGGTCTCTGCCAGTTCTCAGAGAAG	60						
Db	105	ATGGAGAGGTGGACATGAATACATACAGGACAGGTCTCTGCCAGTTCTCAGAGAAG	164						
QY	61	TACAAGCAAGTCTACTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA	120						
Db	165	TACAAGCAAGTCTACTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA	224						
QY	121	AATGCACTGCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGAGCTGCGCACACC	180						
Db	225	AATGCACTGCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGAGCTGCGCACACC	284						
QY	181	TATCTGCTGAACCTGATGGTGGCCCACTGCTTTATGTGCTATTGCCCTTCTCATCATC	240						
Db	285	TATCTGCTGAACCTGATGGTGGCCCACTGCTTTATGTGCTATTGCCCTTCTCATCATC	344						
QY	241	ACCTACTCACTAGATGACAGGTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGTGCACATC	300						
Db	345	ACCTACTCACTAGATGACAGGTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGTGCACATC	404						
QY	301	CTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCTGACCTGCATCTCTGTGCACAG	360						
Db	405	CTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCTGACCTGCATCTCTGTGCACAG	464						
QY	361	TTCTAGTGTGTGTCACCCACTGTGTGCTGCCCTACCGACCGCAGGATGCCCTGG	420						
Db	465	TTCTAGTGTGTGTCACCCACTGTGTGCTGCCCTACCGACCGCAGGATGCCCTGG	524						
QY	421	CTGGCACAGCAGCACCTGGGCCCTGTGTGCTCCAGCTGCTGCCACACTGCGCTTC	480						
Db	525	CTGGCACAGCAGCACCTGGGCCCTGTGTGCTCCAGCTGCTGCCACACTGCGCTTC	584						
QY	481	TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGAGAGAT	540						
Db	585	TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGAGAGAT	644						
QY	541	TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATTTCTGGCTTTCTTCCCTCCTT	600						
Db	645	TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATTTCTGGCTTTCTTCCCTCCTT	704						
QY	601	GCTCATTTTGTGTGCTATTACTCATGTGTGAGAGCCTGATCAAGCCAGAGGAGAACT	660						
Db	705	GCTCATTTTGTGTGCTATTACTCATGTGTGAGAGCCTGATCAAGCCAGAGGAGAACT	764						
QY	661	CATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCCATCTCTACTGCTGTGG	720						
Db	765	CATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCCATCTCTACTGCTGTGG	824						
QY	721	CCTCTTCACTCTGTTTGTGCTTCCATATCATCTGCTCTCTCTACCTCACCACCTG	780						
Db	825	CCTCTTCACTCTGTTTGTGCTTCCATATCATCTGCTCTCTCTACCTCACCACCTG	884						
QY	781	CTTTCTGCTTTCTCAGGACTCGAGCTCTTGATGCGAGCCAGCTGCGCTCAAGATATG	840						
Db	885	CTTTCTGCTTTCTCAGGACTCGAGCTCTTGATGCGAGCCAGCTGCGCTCAAGATATG	944						
QY	841	GAGGCTCTGCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTTCTTTTCAAGGGG	900						
Db	945	GAGGCTCTGCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTTCTTTTCAAGGGG	1004						
QY	901	GGCAAAATAGAGTCAGGCTCTCAGAAACTGAGGCGAGAACAGTTGGGTGAGCATCCA	960						
Db	1005	GGCAAAATAGAGTCAGGCTCTCAGAAACTGAGGCGAGAACAGTTGGGTGAGCATCCA	1064						
QY	961	CTGGGAGGAGAGATGCCCGGTTGACAGATCTGGGTAA	1002						
Db	1065	GCTGGGAGGAGAGATGCCCGGTTGACAGATCTGGGTAA	1106						

ADC86166										
ID	ADC86166 standard; DNA; 1334 BP.									
XX										
AC	ADC86166;									
XX										
DT	01-JAN-2004 (first entry)									
XX										
XX	Human GPCR gene SEQ ID NO:619.									
DE										
XX	ds; gene; human; GPCR;									
KW	guanosine triphosphate-binding protein coupled receptor; gene therapy.									
XX										
OS	Homo sapiens.									
XX										
PN	EP1270724-A2.									
XX										
PD	02-JAN-2003.									
XX										
PF	18-JUN-2002; 2002EP-00013517.									
XX										
PR	18-JUN-2001; 2001JP-00246789.									
XX										
PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.									
PA	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.									
XX										
PI	Suwa M, Asai K, Akiyama Y, Aburatani H;									
XX										
DR	WPI; 2003-315783/31.									
DR	P-PSDB; ADC86167.									
XX										
PT	New polynucleotide, useful for preparing a composition for treating a									
PT	patient in need of increased or suppressed activity or expression of the									
PT	guanosine triphosphate-binding protein coupled receptor.									
XX										
PS	Claim 1; SEQ ID NO 619; 28pp; English.									
XX										
CC	The invention relates to a novel polynucleotide encoding a guanosine									
CC	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of									
CC	the invention may have a use in gene therapy. The polynucleotide and									
CC	polypeptide are useful for preparing a composition for treating a patient									
CC	in need of increased or suppressed activity or expression of the									
CC	guanosine triphosphate-binding protein coupled receptor. The									
CC	polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the									
CC	invention.									
XX										
SQ	Sequence 1334 BP; 283 A; 368 C; 348 G; 335 T; 0 U; 0 Other;									
Query Match	99.8%; Score 1000.4; DB 10; Length 1334;									
Best Local Similarity	99.9%; Pred. No. 2.3e-262;									
Matches 1001;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	ATGGAGAAGTGGACATGAATACATACAGGAAACAGGTCTCTGCCAGTTCTCAGAGAAG	60							
Db	201	ATGGAGAAGTGGACATGAATACATACAGGAAACAGGTCTCTGCCAGTTCTCAGAGAAG	260							
QY	61	TACAAGCAAGTCTACTCTCCCTGGCCTACAGTATCATCTTTATCTAGGGCTGCCACTA	120							
Db	261	TACAAGCAAGTCTACTCTCCCTGGCCTACAGTATCATCTTTATCTAGGGCTGCCACTA	320							
QY	121	AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC	180							
Db	321	AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC	380							
QY	181	TATCTGCTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC	240							
Db	381	TATCTGCTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC	440							
QY	241	ACCTACTCACTAGATGACAGGTGCGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC	300							
Db	441	ACCTACTCACTAGATGACAGGTGCGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC	500							
QY	301	CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG	360							

Db 501 CTGTTCTATACAACTTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACGAG 560
Qy 361 TTCCTAGGTGTGCCACCACTGTGTGCTGCTGCCCTACCGGACCCGCGAGCATGCTCTGG 420
Db 561 TTCCTAGGTGTGCCACCACTGTGTGCTGCTGCCCTACCGGACCCGCGAGCATGCTCTGG 620
Qy 421 CTGGGCACCAACCACTGGGCTGTGTGCTGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 621 CTGGGCACCAACCACTGGGCTGTGTGCTGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 680
Qy 481 TCCACACGGGACTACATCAATGGGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 681 TCCACACGGGACTACATCAATGGGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 740
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 741 TTTGATCGGCTTTTGGCTACGGCATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
Qy 601 GGTCAATTTTGTGTGCTATTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 801 GGTCAATTTTGTGTGCTATTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 860
Qy 661 CATGAGGACGGCAACACAGCCGAGCGAGCTCCATCCGACCATCTCTACTGTGTGTGG 720
Db 861 CATGAGGACGGCAACACAGCCGAGCGAGCTCCATCCGACCATCTCTACTGTGTGTGG 920
Qy 721 CCTCTTCACTCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 921 CCTCTTCACTCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
Qy 781 CTCTTCTGCTTCTCAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 981 CTCTTCTGCTTCTCAGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1040
Qy 841 GAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 1041 GAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100
Qy 901 GGCAAAATAGAGTCAGGCTCTCTCAGAACTGAGGAGCAACAGTGTGGGTGAGCATCCA 960
Db 1101 GGCAAAATAGAGTCAGGCTCTCTCAGAACTGAGGAGCAACAGTGTGGGTGAGCATCCA 1160
Qy 961 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1002
Db 1161 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1202

RESULT 4

AAS17746

AC AAS17746 standard; DNA; 3143 BP.

XX AC AAS17746;

XX AC AAS17746;

DT 26-FEB-2002 (first entry)

XX Human genomic clone for P2Y-like G protein-coupled receptor.

XX Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD;
KW chronic obstructive pulmonary disease; nervous system disease;
KW Parkinson's disease; multiple sclerosis; dementia; stroke;
KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;
KW bacterial infection; fungal infection; protozoan infection;
KW viral infection; pain; cancer; anorexia; bulimia; asthma;
KW acute heart failure; hypertension; hypertension; osteoporosis; diabetes;
KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; delirium; severe mental retardation; dyskinesia.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 520..2498

FT /*tag= a

FT XX /product= "P2Y-like GPCR"
XX WO200185764-A2.
XX PD 15-NOV-2001.
XX PF 09-MAY-2001; 2001WO-EP005244.
XX PR 11-MAY-2000; 2000US-0203582P.
XX PR 21-FEB-2001; 2001US-0269857P.
XX (FARB) BAYER AG.
XX Ramakrishnan S;
PI WPI; 2002-075242/10.
XX DR P-PSDB; AAU11251.
XX New polynucleotides for producing P2Y-like G protein-coupled receptors (GPCR) that are used for screening inhibitors or regulators of human P2Y-like GPCR, especially useful for treating pain, cancer or neurological disorders.
XX Disclosure; Fig 1; 114pp; English.
XX The invention relates to an isolated polynucleotide encoding a P2Y-like G protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or allele, a host cell containing an expression vector comprising the polynucleotide and screening for agents that regulate the GPCR activity. The polynucleotide is useful for producing P2Y-like GPCR polypeptide, which may be employed for screening agents that inhibit or regulate human P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is useful for treating or ameliorating P2Y-like GPCR disorders, particularly COPD (chronic obstructive pulmonary disease), peripheral or central nervous system disease (e.g. Parkinson's disease, multiple sclerosis, dementia, stroke, Alzheimer's disease and many other diseases and disorders listed in the specification), benign prostatic hyperplasia or urinary incontinence. A pharmaceutical composition containing the modulators and/or regulators of P2Y-like GPCR is useful for modulating the activity of a P2Y-like GPCR. In particular, these are useful for treating, preventing or ameliorating infections (e.g. bacterial, fungal, protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma, acute heart failure, hypertension, hypertension, osteoporosis, diabetes, angina pectoris, myocardial infarction, ulcers, inflammation, allergies, psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic depression, delirium, severe mental retardation or dyskinesias). The present sequence is a genomic clone encoding the P2Y-like GPCR of the invention
XX SQ Sequence 3143 BP; 818 A; 771 C; 726 G; 828 T; 0 U; 0 Other;
Query Match 99.8%; Score 1000.4; DB 6; Length 3143;
Best Local Similarity 99.9%; Pred. No. 3.4e-262;
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGAGAAGGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTCTCTCAGAGAAG 60
Db 520 ATGGAGAAGGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTCTCTCAGAGAAG 579
Qy 61 TACAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
Db 580 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGCTGCCACTA 639
Qy 121 AATGGCACTCTCTTTGTGGCACTTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACCACC 180
Db 640 AATGGCACTCTCTTTGTGGCACTTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACCACC 699
Qy 181 TATCTGGTGAACCTGATGTGGCGGACCTCTCTTTATGTGTGCTATTGCCCTTCTCATCATC 240
Db 700 TATCTGGTGAACCTGATGTGGCGGACCTCTCTTTATGTGTGCTATTGCCCTTCTCATCATC 759
Qy 241 ACCTACTCTAGTATGACAGGTGGCCCTTCGGGAGCTGCTTGCAGAGCTGGTGCATTC 300


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Db 760 ACCTACTCACTAGATGACAGGTGGCCCTTCGCGGAGCTGCTCTGCAAGCTGGTGCACTTC 819
Qy 301 CTGTTCTATATCAACCTTTAGCGAGCATCTGCTGCTGACCTGATCTCTGTGCACGAG 360
Db 820 CTGTTCTATATCAACCTTTAGCGAGCATCTGCTGCTGACCTGATCTCTGTGCACGAG 879
Qy 361 TTCTAGGTGTGTGTCACCACTGTTGCTGCTGCTTACCGGACCCGAGGACATGCTCTGG 420
Db 880 TTCTAGGTGTGTGTCACCACTGTTGCTGCTGCTTACCGGACCCGAGGACATGCTCTGG 939
Qy 421 CTGGGACACAGACCACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 940 CTGGGACACAGACCACTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 999
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGTTATGATGATGATGATGATGATGAT 540
Db 1000 TCCACACGGACTACATCAATGGCCAGATGATCTGTTATGATGATGATGATGATGATGAT 1059
Qy 541 TTGATCGCTTTTGGCTAGGATAGTCTGACATGCTGCTGCTTCTGCTTCTGCTTCTGCT 600
Db 1060 TTGATCGCTTTTGGCTAGGATAGTCTGACATGCTGCTGCTTCTGCTTCTGCTTCTGCT 1119
Qy 601 GGTCAATTTGGTGTCTATTCACTGATGCTCAGGACCTGATCAAGCCAGAGGAGAACCT 660
Db 1120 GGTCAATTTGGTGTCTATTCACTGATGCTCAGGACCTGATCAAGCCAGAGGAGAACCT 1179
Qy 661 CATGAGGACGAGCAACACAGCCGAGGACGCTGATCCATCCGAGCATCTCTACTGTTGTGG 720
Db 1180 CATGAGGACGAGCAACACAGCCGAGGACGCTGATCCATCCGAGCATCTCTACTGTTGTGG 1239
Qy 721 CCTCTTCACTCTGTTTGTGCTTCCATATCACTGCTGCTTCTACCTCACCACCTG 780
Db 1240 CCTCTTCACTCTGTTTGTGCTTCCATATCACTGCTGCTTCTACCTCACCACCTG 1299
Qy 781 CTTTCTGCTTCTCAGGACTGCCAGCTCTTGATGCGCAGCAGTGTGGCTCAAGATATG 840
Db 1300 CTTTCTGCTTCTCAGGACTGCCAGCTCTTGATGCGCAGCAGTGTGGCTCAAGATATG 1359
Qy 841 GAGGCTCTGTGATGTGAGCAGCTGCTCAACCCAGTCTGTACTTCTTTCAAGGGG 900
Db 1360 GAGGCTCTGTGATGTGAGCAGCTGCTCAACCCAGTCTGTACTTCTTTCAAGGGG 1419
Qy 901 GGCAAAATAGAGTCAGCTCTCTCAGAACTGAGGAGAGACAGTGTGGTGAGATCCA 960
Db 1420 GGCAAAATAGAGTCAGCTCTCTCAGAACTGAGGAGAGACAGTGTGGTGAGATCCA 1479
Qy 961 CTGGGAGGAGAGATGCCAGGTTGAACAGATCTGGGTAA 1002
Db 1480 CTGGGAGGAGAGATGCCAGGTTGAACAGATCTGGGTAA 1521
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RESULT 5

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ABQ76000
ID ABQ76000 standard; DNA; 1082 BP.
XX AC ABQ76000;
XX AC ABQ76000;
XX DT 17-OCT-2002 (first entry)
XX DE Human GPCR designated PFI-020 encoding sequence.
XX KW Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;
KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;
KW disorder; PFI-020; gene; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 1..1080
XX FT /*tag= a
XX FT /partial
XX FT /product= "GPCR designated PFI-020"
XX FT /note= "no stop codon given"
```

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XX EP1215214-A1.
PN 19-JUN-2002.
XX 04-DEC-2001; 2001EP-00310137.
XX 18-DEC-2000; 2000GB-00030855.
XX 17-JAN-2001; 2001GB-00001222.
XX (PFI2 ) PFIZER LTD.
XX (PFI2 ) PFIZER INC.
XX FidoCK MD;
XX WPI; 2002-510798/55.
XX P-PSDB; ABB98145.
XX New polynucleotide encoding G protein-coupled receptor PFI-020, useful
XX e.g. for treating eating and sleeping disorders and for identifying
XX specific modulators.
XX Claim 1 (c); Page 11; 23pp; English.
XX The invention relates to an isolated polynucleotide encoding a novel
XX polypeptide belonging to the class of proteins known as G-protein coupled
XX receptors (GPCRs). The activity of proteins of the invention may be
XX described as, antidepressant and neuroleptic. Polynucleotides of the
XX invention are used for recombinant expression of the G protein-coupled
XX receptor (PFI-020) polypeptides, to create transgenic animals, as source
XX of primers, probes, antisense sequences and ribozymes and in gene
XX therapy. Therapeutic agents of the invention can be used to treat a wide
XX range of disorders, particularly mood disorders, depression or arousal,
XX especially eating and sleeping disorders. The current sequence represents
XX a coding sequence for a human GPCR designated PFI-020
XX
XX Sequence 1082 BP; 218 A; 318 C; 277 G; 269 T; 0 U; 0 Other;
```

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Query Match 99.4%; Score 996.4; DB 6; Length 1082;
Best Local Similarity 99.9%; Pred. No. 2.6e-261;
Matches 997; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAGAGAGGTGGACATGATATACATACAGAAACAAGGTCTCTGCGAGTCTCTCAGAGAG 60
Db 85 ATGAGAGAGGTGGACATGATATACATACAGAAACAAGGTCTCTGCGAGTCTCTCAGAGAG 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTTATCTTAGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTTATCTTAGGCTGCCACTA 204
Qy 121 AATGGCACTGTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGGCCACCACC 180
Db 205 AATGGCACTGTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGGCCACCACC 264
Qy 181 TATCTGTGAACCTGATGTTGGCGACCTGCTTTATGTGCTATTGCTCTCTCATCATC 240
Db 265 TATCTGTGAACCTGATGTTGGCGACCTGCTTTATGTGCTATTGCTCTCTCATCATC 324
Qy 241 ACCTACTCACTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCACTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTAGCGAGCATCTGCTGCTGACCTGATCTCTGTGCACGAG 360
Db 385 CTGTTCTATATCAACCTTTAGCGAGCATCTGCTGCTGACCTGATCTCTGTGCACGAG 444
Qy 361 TTCCTAGGTGTGTCACCACTGTTGCTGCTTACCGGACCCGAGGACATGCTCTGG 420
Db 445 TTCCTAGGTGTGTCACCACTGTTGCTGCTTACCGGACCCGAGGACATGCTCTGG 504
Qy 421 CTGGGACACGAGCACCACCTGGGCTGCTGCTGCTCTCAGAGTGTGCTGCCACACTGSCCTTC 480
Db 505 CTGGGACACGAGCACCACCTGGGCTGCTGCTGCTCTCAGAGTGTGCTGCCACACTGSCCTTC 564
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QY 481 TCCACACGGACTACATCAATGATGCGCAGATGATCTGGTATGACATGACAGCCACAGAAAT 540
DB 565 TCCACACGGACTACATCAATGATGCGCAGATGATCTGGTATGACATGACAGCCACAGAAAT 624
QY 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTTTCTTTCCCTCCTT 600
DB 625 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTTTCTTTCCCTCCTT 684
QY 601 GGTCAATTTGGTGTGCTATTCTCACTGATGGTCAGAGCCTGATCAAGCCAGAGGAGAACCT 660
DB 685 GGTCAATTTGGTGTGCTATTCTCACTGATGGTCAGAGCCTGATCAAGCCAGAGGAGAACCT 744
QY 661 CATGAGACAGGCAACACAGCCGAGCGAGTCCATCGGACCATCTACTGTTGTTGG 720
DB 745 CATGAGACAGGCAACACAGCCGAGCGAGTCCATCGGACCATCTACTGTTGTTGG 804
QY 721 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCACTCCACCATCTG 780
DB 805 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCACTCCACCATCTG 864
QY 781 CTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGGCCAGCGAGTGTGGCTACAGATATG 840
DB 865 CTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGGCCAGCGAGTGTGGCTACAGATATG 924
QY 841 GAGCCCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGGGG 900
DB 925 GAGCCCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGGGG 984
QY 901 GGCAAAAATAGAGTCAGCTCTCTCAGAACTGAGGAGCAGAACTGGTGGTGGAGCATCCA 960
DB 985 GGCAAAAATAGAGTCAGCTCTCTCAGAACTGAGGAGCAGAACTGGTGGTGGAGCATCCA 1044
QY 961 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTCG 998
DB 1045 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTCG 1082

RESULT 6
AAS98135
ID AAS98135 standard; DNA; 1063 BP.
AC AAS98135;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human DNA for potential G protein-coupled receptor #92.
XX
KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;
KW Alzheimer's disease; ankyrotrophic lateral sclerosis; asthma;
KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;
KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
KW tuberculosis; cognition disorder; memory disorder; anorexia;
KW hormonal release disorder; cardiovascular activity disorder;
KW pain perception disorder; obesity; diabetes; diabetes; obesity; diabetes;
KW hyperlipidaemia; stroke; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200185791-A1.
XX
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US015332.
XX
PR 11-MAY-2000; 2000US-0203217P.
PR 18-MAY-2000; 2000US-0205945P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX

PI Brown JP, Miller M, Burner G, Fabre-Suver C, Pritchard D;
XX WPI; 2002-066595/09.

Novel G protein-coupled receptor polypeptides including galanin receptor
PT polypeptides useful for identifying modulators that are useful for
PT treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,
PT stroke.

XX Claim 2; Page 98; 144pp; English.

XX The invention relates to an isolated polypeptide encoded by a nucleic
CC molecule that is at least 80% identical to the G protein-coupled
CC (GPCR) polynucleotides included in the specification. Also included are
CC probes based on the GPCR sequences (including antisense probes), a host
CC cell comprising an expression vector comprising the GPCR sequence,
CC antibodies raised against the polypeptides, and methods of identifying
CC modulators of the polypeptides. The polypeptides are useful for
CC identifying modulator compounds which function as modulators, activators,
CC repressors, agonists or antagonists of the novel GPCR polypeptides
CC including the GAL4 polypeptide. The antibodies and nucleic acid probes as
CC described above can be used to detect the presence of the polypeptides
CC and nucleic acids and are used to diagnose a variety of diseases or
CC disorders in which GPCRs are involved e.g., Alzheimer's disease,
CC anyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell
CC carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic
CC obstructive pulmonary disease, Crohn's disease, depression, epilepsy,
CC macular degeneration, lymphoma, melanoma, multiple sclerosis,
CC osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid
CC arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other
CC diseases listed in the specification. The probes and antibodies are also
CC useful for diagnosing cognition and memory disorders, pain perception
CC release disorders, cardiovascular activity disorders, pain perception
CC disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds
CC that decrease or increase the expression of galanin receptor (GALA) can
CC be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR
CC nucleic acid is useful for treating the above mentioned disorders by gene
CC therapy techniques. The present sequence is a novel GPCR polynucleotide
CC of the invention

XX SQ Sequence 1063 BP; 216 A; 315 C; 272 G; 260 T; 0 U; 0 Other;

Query Match 98.1%; Score 983.4; DB 6; Length 1063;
Best Local Similarity 99.8%; Pred. No. 9.1e-258;
Matches 995; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ATGGAGAAAGTGGACATGAATACATACACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 60
DB 67 ATGGAGAAAGTGGACATGAATACATACACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 126
QY 61 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGCTGCCACTA 120
DB 127 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGCTGCCACTA 186
QY 121 AATGGCACTCTCTGTGGCACTTCTGGGGCCCAACCAAGCGCTGGAGCTGTGCCACACC 180
DB 187 AATGGCACTCTCTGTGGCACTTCTGGGGCCCAACCAAGCGCTGGAGCTGTGCCACACC 246
QY 181 TATCTGGTGAACCTGTATGGTGGCCGACCTGTCTTTATGTGCTATTGCCCTTCTCATCATC 240
DB 247 TATCTGGTGAACCTGTATGGTGGCCGACCTGTCTTTATGTGCTATTGCCCTTCTCATCATC 306
QY 241 ACCTACTCACTAGATGACAGGTGGCCCTTGGGGAGCTGTCTGCAAGCTGGTGCACTTC 300
DB 307 ACCTACTCACTAGATGACAGGTGGCCCTTGGGGAGCTGTCTGCAAGCTGGTGCACTTC 366
QY 301 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGTACCTGTCTCTGTGCACCAAG 360
DB 367 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGTACCTGTCTCTGTGCACCAAG 426
QY 361 TTCTAGGTGTGTGCCACCCCACTGTGTTCGCTGCCCTACCGGACCCCGAGCATGCTCTGG 420
DB 427 TTCTAGGTGTGTGCCACCCCACTGTGTTCGCTGCCCTACCGGACCCCGAGCATGCTCTGG 486


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PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267803P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 30-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313930P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTA K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
PI Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA,
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;

PI 08-FEB-2001; 2001US-0267459P.
PI 09-FEB-2001; 2001US-0267803P.
PI 15-FEB-2001; 2001US-0268974P.
PI 26-FEB-2001; 2001US-0271664P.
PI 27-FEB-2001; 2001US-0271839P.
PI 27-FEB-2001; 2001US-0271855P.
PI 02-MAR-2001; 2001US-0272788P.
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PI 20-MAR-2001; 2001US-0278652P.
PI 26-MAR-2001; 2001US-0278775P.
PI 26-MAR-2001; 2001US-0278778P.
PI 29-MAR-2001; 2001US-0279882P.
PI 29-MAR-2001; 2001US-0279884P.
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PI 11-APR-2001; 2001US-0282992P.
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PI 20-APR-2001; 2001US-0285133P.
PI 23-APR-2001; 2001US-0285749P.
PI 03-MAY-2001; 2001US-0288327P.
PI 03-MAY-2001; 2001US-0288504P.
PI 30-MAY-2001; 2001US-0294047P.
PI 30-MAY-2001; 2001US-0294473P.
PI 08-JUN-2001; 2001US-0296964P.
PI 18-JUN-2001; 2001US-0298959P.
PI 19-JUN-2001; 2001US-0299324P.
PI 13-AUG-2001; 2001US-0312020P.
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PI 16-AUG-2001; 2001US-0312908P.
PI 21-AUG-2001; 2001US-0313930P.
PI 28-AUG-2001; 2001US-0315470P.
PI 31-AUG-2001; 2001US-0316447P.
PI 07-SEP-2001; 2001US-0318115P.
PI 07-SEP-2001; 2001US-0318118P.
PI 12-SEP-2001; 2001US-0318740P.
PI 19-SEP-2001; 2001US-0323379P.
PI 18-OCT-2001; 2001US-0330245P.
PI 18-OCT-2001; 2001US-0330308P.
PI 14-NOV-2001; 2001US-0332701P.
PI (TCHE/) TCHERNEV V T.
PI (SPYT/) SPYTEK K A.
PI (ZERH/) ZERHUSEN B D.
PI (PATT/) PATTURAJAN M.
PI (SHIM/) SHIMKETS R A.
PI (LILL/) LI L.
PI (GANG/) GANGOLLI E A.
PI (PADI/) PADIGARU M.
PI (ANDE/) ANDERSON D W.
PI (RAST/) RASTELLI L.
PI (MILL/) MILLER C E.
PI (GERL/) GERLACH V.
PI (TAUP/) TAUPIER R J.
PI (GUSE/) GUSEV V Y.
PI (COLM/) COLMAN S D.
PI (WOLE/) WOLENC A R.
PI (PENA/) PENNA C E A.
PI (FURT/) FURTA K.
PI (GROS/) GROSSE W M.
PI (ALSO/) ALSOBROOK J P.
PI (LEPL/) LEPLEY D M.
PI (RIEG/) RIEGER D K.
PI (BURG/) BURGESS C E.
PI Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA,
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;

PI Gerlach V, Taupier RJ, Gusev VV, Colman SD, Wolenc AR, Pena CEA;
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
DR WPI; 2004-180039/17.
DR P-PSDB; ADN42284.
XX Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX Claim 9; SEQ ID NO 165; 1309pp; English.
XX The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
CC vector, an antibody that binds immunospecifically to NOVX, determining
CC the presence or amount of NOVX in a sample, determining the presence or
CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
CC modulating the activity of NOVX, treating or preventing a NOVX-associated
CC disorder, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX and treating a pathological state
CC in a mammal comprising administering a polypeptide which is at least 95%
CC identical to NOVX (or fragment). NOVX and NA may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
CC detecting the presence of NOVX in samples (e.g. by enzyme linked
CC immunosorbant assay (ELISA). The agents and methods may be used in this
CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
CC and/or atherosclerosis. The present sequence encodes a NOVX protein.
XX SQ Sequence 1108 BP; 225 A; 321 C; 285 G; 277 T; 0 U; 0 Other;

Query Match 97.5%; Score 977.4; DB 12; Length 1108;
Best Local Similarity 99.7%; Pred. No. 4e-256;
Matches 1000; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 ATGGAGAAGGTGGACATGAATACATACAGAGAACAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 96 ATGGAGAAGGTGGACATGAATACATACAGAGAACAGGTCTCTGCCAGTTCTCAGAGAAG 155
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 156 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 215
Qy 121 AATGGCACTGCTTTGTGGCACTTCTGGGGGCCAAACCAAGCGCTGGAGCTGCCACCAACC 180
Db 216 AATGGCACTGCTTTGTGGCACTTCTGGGGGCCAAACCAAGCGCTGGAGCTGCCACCAACC 275
Qy 181 TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCTTATGCTTCCCTTCTCATCATC 240
Db 276 TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCTTATGCTTCCCTTCTCATCATC 335
Qy 241 ACCTACTACTAGATGACAGGTGGCCCTTCTGGGGAGCTCTCGCAAGCTGGTGACATTC 300
Db 336 ACCTACTACTAGATGACAGGTGGCCCTTCTGGGGAGCTCTCGCAAGCTGGTGACATTC 395
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGCATCTCTGTGCACCAG 360
Db 396 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGCATCTCTGTGCACCAG 455
Qy 361 TTCTTAGGTGTGTCACCCACTGTGTTGCTGTCCTTACCGGACCCCGAGGATGCTCTGG 420
Db 456 TTCTTAGGTGTGTCACCCACTGTGTTGCTGTCCTTACCGGACCCCGAGGATGCTCTGG 515
Qy 421 CTGGGCACACAGCACCCTGGGCCCTTGGTGTCTCTCCAGCTGCTGCCACACTGGCCTTC 480
Db 516 CTGGGCACACAGCACCCTGGGCCCTTGGTGTCTCTCCAGCTGCTGCCACACTGGCCTTC 575
Qy 481 TCCACACGGGACTACATCAATGGGCAGATGATCTGGTATGACATGACACCGACCAAGAGAAT 540
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Db 576 TCCACACGGACTACATCAATGCGCAGATGATCTGGTATGACATGACCGACGAGAAAT 635
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTGCTTTTCTTCCCTCCTT 600
Db 636 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTGCTTTTCTTCCCTCCTT 695
Qy 601 GGTCAATTTTGTGTGCTATTCTACATGATGGTCAGAGCCTGATCAAGCCAGAGGAAACCT 660
Db 696 GGTCAATTTTGTGTGCT-TATTCACTGATGGTCAGAGCCTGATCAAGCCAGAGGAAACCT 754
Qy 661 CATGAGACAGGCAACACAGCCAGCCAGAGTCCATCCGACCATCTCTACTGTGTGTGG 720
Db 755 CATGAGACAGGCAACACAGCCAGCCAGAGTCCATCCGACCATCTCTACTGTGTGTGG 814
Qy 721 CCTCTTCAACCTCTGTTTTGTGGCTTCCATATCACTCGCTTCTTCACTTCAACCATCTG 780
Db 815 CCTCTTCAACCTCTGTTTTGTGGCTTCCATATCACTCGCTTCTTCACTTCAACCATCTG 874
Qy 781 CTTTCTGCTTCTCAGAGTCCAGCTCTTGTATGGGAG-CCAGTGTGGCTTACAGATAT 839
Db 875 CTTTCTGCTTCTCAGAGTCCAGCTCTTGTATGGGAGCCAGTGTGGCTTACAGATAT 934
Qy 840 GGAGGCTCTGGTCAGTGTGAGAGTCCCTCAACCCAGTCCCTGCTACTTTTCAAGGG 899
Db 935 GGAGGCTCTGGTCAGTGTGAGAGTCCCTCAACCCAGTCCCTGCTACTTTTCAAGGG 994
Qy 900 GGGCAAAATAGAGTCAAGCTCTCCAGAACTGAGGACAGAACTGGGTGGAGCATCC 959
Db 995 GGGCAAAATAGAGTCAAGCTCTCCAGAACTGAGGACAGAACTGGGTGGAGCATCC 1054
Qy 960 AGCTGGAGGAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1002
Db 1055 AGCTGGAGGAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1097

RESULT 9
ADC25999
ID ADC25999 standard; DNA; 1017 BP.
XX
AC ADC25999;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human purinergic receptor P2Y-related GPCR6 DNA.
XX
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
KW anorectic; cardiant; hypotensive; osteoprotective; anti-ulcer; antiallergic;
KW antiarteriosclerotic; cerebroprotective; antiparkinsonian; G-protein coupled receptor;
KW nootropic; neuroprotective; bacterial infection; immune-related disorder;
KW GPCR; viral; fungal; diabetes; obesity; anorexia; acute heart failure;
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW human; GPCR6; purinergic receptor P2Y; ds; gene.
XX
OS Homo sapiens.
XX
PH Location/Qualifiers
FT 1..1017
FT /*tag= a
FT /product= "Human purinergic receptor P2Y-related GPCR6
FT protein - both "original" and "alternative" versions"
FT /transl_except= (pos:184..186, aa:Pro)
FT /transl_except= (pos:727..729, aa:Xaa)
FT /transl_except= (pos:808..810, aa:Pro)
FT ;note= "Xaa = Unknown; translation exceptions at 184 and
FT 727 are present within "original" protein CDS whilst that
FT at 808 is present within the "alternative" protein CDS"
XX
PN US203088080-A1.
XX
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PD 08-MAY-2003.
XX
PF 21-JUN-2001; 2001US-00885453.
XX
PR 20-JUN-2000; 2000US-0212908P.
PR 05-DEC-2000; 2000EP-00870289.
XX
PA (COMM/) COMMUNI D.
PA (LANN/) LANNY V.
PA (GOVA/) GOVAERTS C.
PA (PARM/) PARMENTIER M.
PA (DETH/) DETHEUX M.
XX
PI Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;
XX
XX WPI; 2003-657983/62.
XX P-PSDB; ADC26000, ADC26009.
XX
XX New human G-protein coupled receptor, useful for treating receptor-
XX mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
XX acute heart failure, osteoporosis, stroke, ulcer, allergy, or
XX neurological disorders.
XX
XX Example 3; Page 15-16; 24pp; English.
XX
XX The invention relates to a novel G-protein coupled receptor (GPCR). The
XX receptor, polynucleotide, agonist, reverse agonist and antagonist of the
XX invention may be useful for treating receptor-mediated disorders
XX including viral, fungal or bacterial infections, immune-related disorders
XX such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
XX hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
XX ulcer and allergy, as well as psychotic and neurological disorders such
XX as schizophrenia and dementia, degenerative diseases such as Parkinson's
XX disease and Alzheimer's disease and dyskinesias such as Huntington's
XX disease. The current sequence is that of the human purinergic receptor
XX P2Y-related GPCR6 DNA of the invention.
XX
XX Sequence 1017 BP; 200 A; 306 C; 252 G; 259 T; 0 U; 0 Other;
XX
XX Query Match 91.9%; Score 920.4; DB 10; Length 1017;
XX Best Local Similarity 99.8%; Pred. No. 1.4e-240;
XX Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 ATGGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 60
Db 85 ATGGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCAAAACCAAGCGCTGGAGCTGGCCACC 180
Db 205 AATGGCACTGTCTTGTGGCACTTCTGGGGCAAAACCAAGCGCTGGAGCTGGCCACC 264
Qy 181 TATCTGGTGAACCTGATGGTGGCGGACCTCTTTATGTGCTATGCGCTTCCCTCATC 240
Db 265 TATCTGGTGAACCTGATGGTGGCGGACCTCTTTATGTGCTATGCGCTTCCCTCATC 324
Qy 241 ACCTACTCTACTAGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCTACTAGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTTATCAACCTTTACGGCAGCATCCTCTGCTGACCTGCACTCTCTGTGCACAG 360
Db 385 CTGTTCTTATCAACCTTTACGGCAGCATCCTCTGCTGACCTGCACTCTCTGTGCACAG 444
Qy 361 TTCTTAGTGTGTGGCCACCACCTGTTGGTGGCTCCCTACCGGACCGGACGATGCTGG 420
Db 445 TTCTTAGTGTGTGGCCACCACCTGTTGGTGGCTCCCTACCGGACCGGACGATGCTGG 504
Qy 421 CTGGGACACGACGACCACTGGGCGCTGGTGGTCTCTCCAGCTGGTCCCACTGGCCCTTC 480
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Db 505 CTGGGCACAGCACCACCTGGTGGCCCTGGTGGTCTCCAGCTGCTGCCACACACTGGCCCTTC 564
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGATGACAGCCAGCAGAGAAAT 540
Db 565 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGATGACAGCCAGCAGAGAAAT 624
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600
Db 625 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTT-TTTCCCTCCTT 683
Qy 601 GGTCAATTTTGGTGTGCTATTACCTGATGGTCAGAGCTTGATCAAGCCAGAGGAGAACTT 660
Db 684 GGTCAATTTTGGTGTGCTATTACCTGATGGTCAGAGCTTGATCAAGCCAGAGGAGAACTT 743
Qy 661 CATGAGACAGGACACAGCCAGCCAGCTCCATCGGACCATCTACTGGTGTGG 720
Db 744 CATGAGACAGGACACAGCCAGCCAGCTCCATCGGACCATCTACTGGTGTGG 803
Qy 721 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCTACCTCACCCTG 780
Db 804 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCTACCTCACCCTG 863
Qy 781 CTCTCTGCTTCTCAGACTGCCAGCTCTTGAATGGCAGCCAGTGTGGCTTACAAGATG 840
Db 864 CTCTCTGCTTCTCAGACTGCCAGCTCTTGAATGGCAGCCAGTGTGGCTTACAAGATG 923
Qy 841 GAGGCTCTGGTGTGAGTGTGAGCAGCTGCTTCAACCCAGTCTGCTACTTCTTCAAGGG 900
Db 924 GAGGCTCTGGTGTGAGTGTGAGCAGCTGCTTCAACCCAGTCTGCTACTTCTTCAAGGG 983
Qy 901 GGCAAAATAGATCAGGCTCTCTCAGAACTGA 934
Db 984 GGCAAAATAGATCAGGCTCTCTCAGAACTGA 1017

RESULT 10

AAD61648
ID AAD61648 standard; DNA; 1017 BP.

AC AAD61648;

DT 15-JAN-2004 (first entry)

XX Human GPCR α 6 DNA.

XX Human; G-protein coupled receptor; GPCR; infection; neoplastic process;
KW inflammation; myocardial infarction; atherosclerosis; angina pectoris;
KW hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;
KW diabetes; cancer; virucide; analgesic; cardiant; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1017

FT /*tag= a

FT /product= "Human GPCR protein"

XX US2003108986-A1.

XX 12-JUN-2003.

XX 20-FEB-2002; 2002US-00079384.

XX 21-JUN-2001; 2001US-00885453.

XX (EURO-) EUROSREEN SA.

XX Communi D, Lannoy V, Brezillon S, Detheux M, Parmentier M;

PI Goovaerts C;

XX WPI; 2003-810852/76.

DR P-PSDB; ABW00804.

PT Novel G-protein coupled receptor useful for treating viral infections,
PT bacterial infections, fungal infections, cancer, diabetes, hypertension,
PT osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.
XX Claim 5; Fig 4; Opp; English.

XX The present invention relates to novel G-protein coupled receptors
CC (GPCRs) and the nucleic acids encoding them. The invention is useful for
CC treating viral, bacterial and fungal infections, inflammatory and
CC neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,
CC angina pectoris, myocardial infarction and atherosclerosis. The present
CC sequence is human G-protein coupled receptor (GPCR) DNA

SQ Sequence 1017 BP; 200 A; 306 C; 252 G; 259 T; 0 U; 0 Other;

Query Match 91.9%; Score 920.4; DB 10; Length 1017;

Best Local Similarity 99.8%; Pred. No. 1.4e-240;

Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ATGAGAGAGGTGGACATGAATACATCACAGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 85 ATGAGAGAGGTGGACATGAATACATCACAGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGCTGCCACTA 204
Qy 121 AATGGCACTCTCTGTGGCACTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACCACC 180
Db 205 AATGGCACTCTCTGTGGCACTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACCACC 264
Qy 181 TATCTGTGAACCTGTATGGTGGCGACCTGCTTTTATGTGCTATTGCTCTCTCATCATC 240
Db 265 TATCTGTGAACCTGTATGGTGGCGACCTGCTTTTATGTGCTATTGCTCTCTCATCATC 324
Qy 241 ACCTACTCCTAGATGACAGGTGGCCCTTCCGGAGCTGCTCTCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCCTAGATGACAGGTGGCCCTTCCGGAGCTGCTCTCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 360
Db 385 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGCTGCTGCTGCTGCTGCTG 444
Qy 361 TTCCTAGTGTGTGCCACCCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 445 TTCCTAGTGTGTGCCACCCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504
Qy 421 CTGGGCAACGACCACTCTGGGCCCTGGTGGTCTCTCAGCTGTGCTGCCACACTGGCTTC 480
Db 505 CTGGGCAACGACCACTCTGGGCCCTGGTGGTCTCTCAGCTGTGCTGCCACACTGGCTTC 564
Qy 481 TCCACACGGACTACATCAATGGCAGATGATCTGGTATGACATGACAGCAGCAGAGAAAT 540
Db 565 TCCACACGGACTACATCAATGGCAGATGATCTGGTATGACATGACAGCAGCAGAGAAAT 624
Qy 541 TTTGATCGGCTTTTGGCTAGCGCATAGTTCTGACATTTGCTGCTTTCTTTCTCTCTT 600
Db 625 TTTGATCGGCTTTTGGCTAGCGCATAGTTCTGACATTTGCTGCTTT-TTTCCCTCTT 683
Qy 601 GGTCAATTTTGGTGTGCTATTACCTAGTGGTCAGGAGCTTGATCAAGCCAGAGGAGAACT 660
Db 684 GGTCAATTTTGGTGTGCTATTACCTAGTGGTCAGGAGCTTGATCAAGCCAGAGGAGAACT 743
Qy 661 CATGAGACAGGCAACACAGCCCGAGCAGGTCCATCGGACCATCTACTGCTGTGTGG 720
Db 744 CATGAGACAGGCAACACAGCCCGAGCAGGTCCATCGGACCATCTACTGCTGTGTGG 803
Qy 721 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTGCTCTCTTACCTCACCCTG 780
Db 804 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTGCTCTCTTACCTCACCCTG 863
Qy 781 CTCTTCTGCTTCTCAGGACTGCCAGCTCTTGAATGGCAGCCAGTGTGGCTTACAAGATG 840

Db	864	CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGCGCTACAAGATATG	923
Qy	841	GAGGCTCTGGTGTGAGTGTGAGCAGTGCCTCAACCCAGTCTCTGTACTTTCTTTCAAGGG	900
Db	924	GAGGCTCTGGTGTGAGTGTGAGCAGTGCCTCAACCCAGTCTCTGTACTTTCTTTCAAGGG	983
Qy	901	GGCAAAATAGAGTCAAGGCTCCTCCAGAACTGA	934
Db	984	GGCAAAATAGAGTCAAGGCTCCTCCAGAACTGA	1017
RESULT 11			
ABQ79300			
ID	ABQ79300 standard; DNA; 1020 BP.		
XX	AC ABQ79300;		
XX	17-OCT-2002 (first entry)		
XX	Human GPCR designated PFI-020' encoding sequence.		
DE	Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;		
XX	Gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;		
KW	disorder; PFI-020'; gene; ds.		
KW	Homo sapiens.		
XX	OS		
XX	Key		
FH	CDS		
FT	1..1020		
FT	/*tag= a		
FT	/product= "GPCR designated PFI-020"		
XX	EP1215214-A1.		
XX	19-JUN-2002.		
XX	04-DEC-2001; 2001EP-00310137.		
XX	18-DEC-2000; 2000GB-00030855.		
PR	17-JAN-2001; 2001GB-00001222.		
XX	(PFI2) PFIZER LTD.		
PA	(PFI2) PFIZER INC.		
XX	Fidock MD;		
PI	WPI; 2002-510798/55.		
XX	P-PSDB; ABB98146.		
DR	New polynucleotide encoding G protein-coupled receptor PFI-020, useful		
XX	e.g. for treating eating and sleeping disorders and for identifying		
PT	specific modulators.		
PT	Claim 1 (d); Page 12; 23pp; English.		
XX	The invention relates to an isolated polynucleotide encoding a novel		
CC	polypeptide belonging to the class of proteins known as G-protein coupled		
CC	receptors (GPCRs). The activity of proteins of the invention may be		
CC	described as, antidepressant and neuroleptic. Polynucleotides of the		
CC	invention are used for recombinant expression of the G protein-coupled		
CC	receptor (PFI-020) polypeptides, to create transgenic animals, as source		
CC	of primers, probes, antisense sequences and ribozymes and in gene		
CC	therapy. Therapeutic agents of the invention can be used to treat a wide		
CC	range of disorders, particularly mood disorders, depression or arousal,		
CC	especially eating and sleeping disorders. The current sequence represents		
CC	a coding sequence for a human GPCR designated PFI-020'		
XX	Sequence 1020 BP; 200 A; 309 C; 252 G; 259 T; 0 U; 0 Other;		
SQ			
Query Match 91.5%; Score 917.2; DB 6; Length 1020;			
Best Local Similarity 99.5%; Pred. No. 1.1e-239;			
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;			

Qy	1	ATCGAGAGGTGACATGATATACATCACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG	60
Db	85	ATCGAGAGAGGTGACATGATATACATCACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG	144
Qy	61	TACAAGCAAGTCTACCTCTCCCTGGGCTACAGATATCATCTTTATCTTAGGGCTGCCACTA	120
Db	145	TACAAGCAAGTCTACCTCTCCCTGGGCTACAGATATCATCTTTATCTTAGGGCTGCCACTA	204
Qy	121	AATGGCACTGTCTTTGTGGCACTTTCTGGGGCAAAACCAAGCGCTGGAGCTGTGCCACACC	180
Db	205	AATGGCACTGTCTTTGTGGCACTTTCTGGGGCAAAACCAAGCGCTGGAGCTGTGCCACACC	264
Qy	181	TATCTGGTGAACCTGTATGGTGGCGGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATC	240
Db	265	TATCTGGTGAACCTGTATGGTGGCGGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATC	324
Qy	241	ACCTACTCACTAGATGACAGGTGGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC	300
Db	325	ACCTACTCACTAGATGACAGGTGGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC	384
Qy	301	CTCTTCTATATCAACCTTTACGGCAGCATCCTGCTGACCTGACATCTCTGTGCACAG	360
Db	385	CTCTTCTATATCAACCTTTACGGCAGCATCCTGCTGACCTGACATCTCTGTGCACAG	444
Qy	361	TTCTTAGGTGTGGCCACCCACTGTGTGGTGGCTCCCTACCGGACCCGCGAGCATGCTGG	420
Db	445	TTCTTAGGTGTGGCCACCCACTGTGTGGTGGCTCCCTACCGGACCCGCGAGCATGCTGG	504
Qy	421	CTGGGACACGACACCACTGGGCTGGTGGTCTCTCAGCTGCTGCCACACTGGCCCTTC	480
Db	505	CTGGGACACGACACCACTGGGCTGGTGGTCTCTCAGCTGCTGCCACACTGGCCCTTC	564
Qy	481	TCCCAACGGACTACATCAATATGCGCAGATGATCTGTATGACATGACACGACCAAGAAAT	540
Db	565	TCCCAACGGACTACATCAATATGCGCAGATGATCTGTATGACATGACACGACCAAGAAAT	624
Qy	541	TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTT--CCCTCC	598
Db	625	TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCC	684
Qy	599	TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAAGGAGCTGATCAAGCCAGAGGAAC	658
Db	685	TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAAGGAGCTGATCAAGCCAGAGGAAC	744
Qy	659	CTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACCACTCTACTGGTGTGT	718
Db	745	CTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACCACTCTACTGGTGTGT	804
Qy	719	GGCCTCTTCACCCCTCTGTTTGTGGCTTCCATATCACTCGCTCCTTCTACCTCACCATC	778
Db	805	GGCCTCTTCACCCCTCTGTTTGTGGCTTCCATATCACTCGCTCCTTCTACCTCACCATC	864
Qy	779	TGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA	838
Db	865	TGCTTTCTGCTTTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA	924
Qy	839	TGAGAGCCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTATCTTTTCAAGG	898
Db	925	TGAGAGCCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTATCTTTTCAAGG	984
Qy	899	GGGGCAAAATAGAGTCAAGCTCCTCCAGAACTGA	934
Db	985	GGGGCAAAATAGAGTCAAGCTCCTCCAGAACTGA	1020
RESULT 12			
AAD29667	ID AAD29667 standard; cDNA; 1076 BP.		
XX	AAD29667;		
XX	17-MAY-2002 (first entry)		
DT			
XX			

Human G-protein coupled receptor (GCRC-1) cDNA.

Human; G-protein coupled receptor; GCRC-1; cell proliferative disorder; neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory; metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease; Pick's disease; Huntington's disease; Parkinson's disease; hypertension; atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS; anemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant; nootropic; neuroprotective; cardiac; immunosuppressive; anorectic; virucide; gene; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 57..1076
/*tag= a
/product= "Human GCRC-1"

W0200210387-A2.

07-FEB-2002.

25-JUL-2001; 2001WO-US023433.

27-JUL-2000; 2000US-0221478P.

03-AUG-2000; 2000US-0223268P.

21-AUG-2000; 2000US-0227054P.

08-SEP-2000; 2000US-0231121P.

13-SEP-2000; 2000US-0232243P.

15-SEP-2000; 2000US-0232691P.

22-SEP-2000; 2000US-0235146P.

(INCY-) INCYTE GENOMICS INC.

Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Wallia NK, Hafalia AJA;
Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Grael RC;
Warren BA, Lee AE, Ding L;

WPI; 2002-188744/24.

P-PSDB; NAE18640.

New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic disorders.

Claim 5; Page 137-138; 150pp; English.

The invention relates to novel human G-protein coupled receptors (GCRC) and their encoding polynucleotides. GCRC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCRC is useful for diagnosing, treating and preventing a cell proliferative disorder (e.g., hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/inflammatory disorder (e.g., acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infections. GCRC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCRC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. GCRC is useful in Southern or Northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays, and in

CC microarrays utilising fluids or tissues from patients to detect altered GCRC expression. The present sequence is human GCRC-1 cDNA

XX Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;

SQ Query Match 91.5%; Score 917.2; DB 6; Length 1076;
Best Local Similarity 99.5%; Pred. No. 1.1e-239;
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ATGGAGAGGTGGACATGATACATACAGGAAAGGTCTCTGCCAGTCTCTCAGAGAG 60
Db 141 ATGGAGAGGTGGACATGATACATACAGGAAAGGTCTCTGCCAGTCTCTCAGAGAG 200

Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGCTGCCACTA 120

Db 201 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGCTGCCACTA 260

Qy 121 AATGGCACTGTCTTGTGGCACTTCTGGGGGCAAAACCAAGCGCTGGAGTGTGCCACACC 180

Db 261 AATGGCACTGTCTTGTGGCACTTCTGGGGGCAAAACCAAGCGCTGGAGTGTGCCACACC 320

Qy 181 TATCTGTGTAACCTGATGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240

Db 321 TATCTGTGTAACCTGATGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 380

Qy 241 ACCTACTCATTAGATGACAGGTGGCCCTTGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300

Db 381 ACCTACTCATTAGATGACAGGTGGCCCTTGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 440

Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGATCTCTGTGACACAG 360

Db 441 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGATCTCTGTGACACAG 500

Qy 361 TTCTAGGTGTGTCACCCACCTGCTTGGTGGCTTACCGGACCGGAGCATGCGCTGG 420

Db 501 TTCTAGGTGTGTCACCCACCTGCTTGGTGGCTTACCGGACCGGAGCATGCGCTGG 560

Qy 421 CTGGGACACGACCACTCTGGGCCCTTGGTGGCTTCTCAGCTGCTGCCACACTGGCTTC 480

Db 561 CTGGGACACGACCACTCTGGGCCCTTGGTGGCTTCTCAGCTGCTGCCACACTGGCTTC 620

Qy 481 TCCACACGGAATACATCAATGGCCAGATGATCTGGTATGACATGACAGCAAGAGAA 540

Db 621 TCCACACGGAATACATCAATGGCCAGATGATCTGGTATGACATGACAGCAAGAGAA 680

Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATGCTGGCTTCTTTT - CCCTCC 598

Db 681 TTTGATCGGCTTTTGGCTACGGCATAGTCTGACATGCTGGCTTCTTTT - CCCTCC 740

Qy 599 TTGTCATTTTGGTGTGCTATTCTAGTGTGAGGAGCTGTGATCAAGCCAGAGAGAA 658

Db 741 TTGTCATTTTGGTGTGCTATTCTAGTGTGAGGAGCTGTGATCAAGCCAGAGAGAA 800

Qy 659 CTGATGAGGACAGCAACACAGCCCGAGCCAGGTCCATCCGAGCATCTACTGTGTGT 718

Db 801 CTGATGAGGACAGCAACACAGCCCGAGCCAGGTCCATCCGAGCATCTACTGTGTGT 860

Qy 719 GGCTCTTCCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCTACTCACCATC 778

Db 861 GGCTCTTCCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTTCTACTCACCATC 920

Qy 779 TGTCTTCTGCTTTCTCAGGACTGCGAGCTCTTGTATGGCAGCGAGTGTGGCTTACAAGATA 838

Db 921 TGTCTTCTGCTTTCTCAGGACTGCGAGCTCTTGTATGGCAGCGAGTGTGGCTTACAAGATA 980

Qy 839 TGGAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGG 898

Db 981 TGGAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGG 1040

Qy 899 GGGGCAAAATAGAGTCAAGCTCTCTCCGAAACTGA 934

Db 1041 GGGGCAAAATAGAGTCAAGCTCTCTCCGAAACTGA 1076

RESULT 13

AD030395
ID AD030395 standard; cDNA; 1076 BP.
XX
AC AD030395;
XX
XX 29-JUL-2004 (first entry)
XX
DE Human GPCR P2Y3L polynucleotide, SEQ ID NO:1498.
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytosatic; antinflammatory; vasotropic; antidiarrhoeic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2004040000-A2;
PN
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
XX
XX 09-SEP-2002; 2002US-0409303P.
PR
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
XX
XX Galitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madison L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
XX WPI; 2004-390329/36.
DR
XX P-PSDB; ADO30394.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
XX Claim 151; SEQ ID NO 1498; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,

anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
obesity, enzyme deficiency-related diseases or vitamin deficiency-related
diseases); and disorders of the kidney, liver, lung, breast, ovary,
uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
nucleic acid of the invention. Note: The full sequence data for this
patent did not form part of the printed specification; those sequences
not shown were obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;
Query Match 91.5%; Score 917.2; DB 12; Length 1076;
Best Local Similarity 99.5%; Pred. No. 1.1e-239;
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

1 ATGGAGAGGTGGACATGAATATACATACAGAACAGGTCTCTGCCAGTTTCTCAGAGAAG 60
141 ATGGAGAGGTGGACATGAATATACATACAGAACAGGTCTCTGCCAGTTTCTCAGAGAAG 200
61 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 120
201 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 260
121 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 180
261 AATGGCACTCTCTTGTGGCACTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 320
181 TATCTGGTGAACCTGATGGTGGCGGACCTCTTTATGTGCTATTCCTTCATCATC 240
321 TATCTGGTGAACCTGATGGTGGCGGACCTCTTTATGTGCTATTCCTTCATCATC 380
241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGTCTGCAAGCTGGTGCACTTC 300
381 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGTCTGCAAGCTGGTGCACTTC 440
301 CTGTTCTATATCAACCTTTACGGCAGCATCCTGCTGTGACCTGCACTCTCTGTGCAACAG 360
441 CTGTTCTATATCAACCTTTACGGCAGCATCCTGCTGTGACCTGCACTCTCTGTGCAACAG 500
361 TTCTTAGGTGTGGCCACCCACTGTGTGCTGGCTACCGGACCCGACGCACTGCTGG 420
501 TTCTTAGGTGTGGCCACCCACTGTGTGCTGGCTACCGGACCCGACGCACTGCTGG 560
421 CTGGGACACGACACCACTCTGGGCCCTCTCCAGCTGTGCTGCCACCACTGGCCTTC 480
561 CTGGGACACGACACCACTCTGGGCCCTCTCCAGCTGTGCTGCCACCACTGGCCTTC 620
481 TCCACACCGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACCGCAAGAAAT 540
621 TCCACACCGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACCGCAAGAAAT 680
541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGTTGCTGCTTTCTTTT -CCCTCC 598
681 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGTTGCTGCTTTCTTTTCCCTCC 740
599 TTGCTCATTTTGGTGTGCTATTCACTGATGGTCAAGGACCTGATCAAGCCAGAGGAAAC 658
741 TTGCTCATTTTGGTGTGCTATTCACTGATGGTCAAGGACCTGATCAAGCCAGAGGAAAC 800
659 CTATGAGGACAGGCAACACAGCCCGAGCCAGGTTCATTCGGGACCATCTCTACTGGTGTGT 718
801 CTATGAGGACAGGCAACACAGCCCGAGCCAGGTTCATTCGGGACCATCTCTACTGGTGTGT 860
719 GGCTCTTTCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTCTTCTACCTCACCATC 778
861 GGCTCTTTCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTCTTCTACCTCACCATC 920
779 TGCTTTCTGCTTTCTCAGGACTGCGAGCTCTTGTATGGCAGCCAGTGTGGCTTACAAGATA 838
921 TGCTTTCTGCTTTCTCAGGACTGCGAGCTCTTGTATGGCAGCCAGTGTGGCTTACAAGATA 980

QY 839 TGGAGGCTCTGGTGAAGTGCAGAGCTGCTCAACCCAGTCCCTGACTCTTTTCAAGG 898
DB 981 TGGAGGCTCTGGTGAAGTGCAGAGCTGCTCAACCCAGTCCCTGACTCTTTTCAAGG 1040
QY 899 GGGGCAAAATAGAGTCAGGCTCTCCAGAACTGA 934
DB 1041 GGGGCAAAATAGAGTCAGGCTCTCCAGAACTGA 1076

RESULT 14

ID AAS17747
XX AAS17747 standard; DNA; 850 BP.

AC AAS17747;

DT 26-FEB-2002 (first entry)

DE Human P2Y-like G protein-coupled receptor exon 1.

XX Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD;
XX Chronic obstructive pulmonary disease; nervous system disease;
XX Parkinson's disease; multiple sclerosis; dementia; stroke;
XX Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;
XX bacterial infection; fungal infection; protozoan infection;
XX viral infection; pain; cancer; anorexia; bulimia; asthma; exon 1;
XX acute heart failure; hypotension; hypertension; osteoporosis; diabetes;
XX angina pectoris; myocardial infarction; ulcer; inflammation; allergy;
XX psychotic disorder; neurological disorder; anxiety; schizophrenia;
XX manic depression; delirium; severe mental retardation; dyskinesia.

XX Homo sapiens.

XX WO200185764-A2.

XX 15-NOV-2001.

XX 09-MAY-2001; 2001WO-EP005244.

XX 11-MAY-2000; 2000US-0203582P.

XX 21-FEB-2001; 2001US-0269857P.

XX (FARB) BAYER AG.

XX Ramakrishnan S;

XX WPI; 2002-075242/10.

XX New polynucleotides for producing P2Y-like G protein-coupled receptors
XX (GPCR) that are used for screening inhibitors or regulators of human P2Y-
XX like GPCR, especially useful for treating pain, cancer or neurological
XX disorders.

XX Claim 1; Fig 4; 114pp; English.

XX The invention relates to an isolated polynucleotide encoding a P2Y-like G
XX protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or
XX allele, a host cell containing an expression vector comprising the
XX polynucleotide and screening for agents that regulate the GPCR activity.
XX The polynucleotide is useful for producing P2Y-like GPCR polypeptide,
XX which may be employed for screening agents that inhibit or regulate human
XX P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is
XX useful for treating or ameliorating P2Y-like GPCR disorders, particularly
XX COPD (chronic obstructive pulmonary disease), peripheral or central
XX nervous system disease (e.g. Parkinson's disease, multiple sclerosis,
XX dementia, stroke, Alzheimer's disease and many other diseases and
XX disorders listed in the specification), benign prostatic hyperplasia or
XX urinary incontinence. A pharmaceutical composition containing the
XX modulators and/or regulators of P2Y-like GPCR is useful for modulating
XX the activity of a P2Y-like GPCR. In particular, these are useful for
XX treating, preventing or ameliorating infections (e.g. bacterial, fungal,
XX protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,
XX acute heart failure, hypotension, hypertension, osteoporosis, diabetes,

CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,
CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic
CC depression, delirium, severe mental retardation or dyskinesia). The
CC present sequence is exon 1 of the P2Y-like GPCR of the invention

XX Sequence 850 BP; 165 A; 262 C; 201 G; 222 T; 0 U; 0 Other;

QY Query Match 84.7%; Score 848.4; DB 6; Length 850;

DB Best Local Similarity 99.9%; Pred. No. 5.9e-221;

XX Matches 849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTGGACATGAATACATACAGAAACAAGGTCTCTCCAGTTCTCAGAGAAG 60

DB 1 ATGGAGAAAGTGGACATGAATACATACAGAAACAAGGTCTCTCCAGTTCTCAGAGAAG 60

QY 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTAGGGCTGCCACTA 120

DB 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTAGGGCTGCCACTA 120

QY 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180

DB 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180

QY 181 TATCTGTGAACCTGTATGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240

DB 181 TATCTGTGAACCTGTATGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240

QY 241 ACCTACTACTAGATGACAGGTGGCCCTTGGGAGCTGCTCTGCNAGCTGGTGCACATTC 300

DB 241 ACCTACTACTAGATGACAGGTGGCCCTTGGGAGCTGCTCTGCNAGCTGGTGCACATTC 300

QY 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGTGCTGTGACCTGCATCTCTGTGCACCAG 360

DB 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGTGCTGTGACCTGCATCTCTGTGCACCAG 360

QY 361 TTCTAGGTGTGTCACCACTCTGTGCTGTGCTTACCGGACCGGAGCATGCTGCTGG 420

DB 361 TTCTAGGTGTGTCACCACTCTGTGCTGTGCTTACCGGACCGGAGCATGCTGCTGG 420

QY 421 CTGGGACACGACCACTGGGCGCTGGTGGTCTCCAGCTGCTGCCACACTGGCCTTC 480

DB 421 CTGGGACACGACCACTGGGCGCTGGTGGTCTCCAGCTGCTGCCACACTGGCCTTC 480

QY 481 TCCACACGGACTACATCAATGGCCAGATGATCTGCTATGACATGACACGACCAAGAGAT 540

DB 481 TCCACACGGACTACATCAATGGCCAGATGATCTGCTATGACATGACACGACCAAGAGAT 540

QY 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTTTCTCCTCTT 600

DB 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTTTCTCCTCTT 600

QY 601 GGTCAATTTGGTGTGCTATTACATGTGCTGAGAGCTGATCAAGCCAGAGAGAACT 660

DB 601 GGTCAATTTGGTGTGCTATTACATGTGCTGAGAGCTGATCAAGCCAGAGAGAACT 660

QY 661 CATCAGACAGGCAACACAGCCGACGAGTCCATCCGACCATCTCTACTGCTGTGG 720

DB 661 CATCAGACAGGCAACACAGCCGACGAGTCCATCCGACCATCTCTACTGCTGTGG 720

QY 721 CCTCTTCACTCTGTTTTGTGGCTTTTCCATATCATCTGCTCTTCTTCTACCATCTG 780

DB 721 CCTCTTCACTCTGTTTTGTGGCTTTTCCATATCATCTGCTCTTCTTCTACCATCTG 780

QY 781 CTTTCTGCTTCTCAGAGCTGCCAGCTCTTGATGGCAGCAGTGTGGCTCTACAGATATG 840

DB 781 CTTTCTGCTTCTCAGAGCTGCCAGCTCTTGATGGCAGCAGTGTGGCTCTACAGATATG 840

QY 841 GAGGCCCTCTG 850

DB 841 GAGGCCCTCTG 850

RESULT 15

AD030397
ID ADO30397 standard; cDNA; 906 BP.
XX
AC ADO30397;
XX
DT 29-JUL-2004 (first entry)
XX
DE Mouse GPCR P2Y3L polynucleotide, SEQ ID NO:1500.
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytosatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
KW murine; gene; ss.
XX
XX Mus musculus.
OS
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
XX
XX 09-SEP-2002; 2002US-0409303P.
PR
PR 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.
PA
XX Gitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
XX WPI: 2004-390329/36.
DR
DR P-PSDB; ADO30396.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
XX Claim 151; SEQ ID NO 1500; 542pp; English.
XX
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid

CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 906 BP; 173 A; 276 C; 216 G; 241 T; 0 U; 0 Other;
Query Match 60.3%; Score 604.6; DB 12; Length 906;
Best Local Similarity 80.8%; Pred. No. 2.2e-154;
Matches 731; Conservative 0; Mismatches 169; Indels 5; Gaps 2;
QY 1 ATGGAGAAGGTGGACATGAATACATACAGAGAAACAAGGCTCTGCCAGTTCTCAGAGAAG 60
DB 1 ATGGAGAGCTAGATATGATGCTCAAGGGTCGTGGCGCCTGCCACTTCTCAGAGAGC 60
QY 61 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
DB 61 TACAAGCAAGTCTACCTATCATTAACCTACAGTCTCATCTTTATGCTAGGGATGCCCTC 120
QY 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAC 180
DB 121 AATGGGGCTGTCTTTATGGCTCTCTGGTGCCAAACCAAGCGCTGGAGCTGTGCCACCAC 180
QY 181 TATCTGGTGAACCTGATGGTGGCGGACCTCTCTTTATGTGCTA---TTGCCCTTCTCTCATC 237
DB 181 TACTGTATGAACCTGGTGGTGGCTGACCTGCTTTATATGCTAAGCCTGCCCTTCTCATC 240
QY 238 ATCACTTACTCTAGATGACAGGTGGCCCTTCGGGGAGCTGTCTTCAAGTGGTGGAC 297
DB 241 ATCACTTACGGCTGGGTGACACCTGGCTCTTTGGGGAGATGCTGTGACAGTTGGTGGC 300
QY 298 TTCTGTCTTATATCAACCTTTAGGGCAGCATCTCTGCTGACCTGACCTCTCTGTGCAC 357
DB 301 TTCTGTCTTACACCAACCTCTACAGCAGCATCTCTGCTGACCTGACCTCTCTCTACAC 360
QY 358 CAGTTCTCTAGGTGTGTGCCACCCACCTGTGTTCGCTGCCCTTACCGGACCCGACGACATGCC 417
DB 361 CGCTTCTTAGAGTGTGCCACCCCTCTGAGCTCACTGTCTTACCGGACTCAACCGCACGCC 420
QY 418 TGGCTGGGACACGACACCACTGGGCGCTGGTGGTCTCTCAGCTGTCTGCCACACTGGCC 477
DB 421 TGGCAGGACGCTGCTGCCACCCCTGGTAGTCTTCCAAATTGCTGGCGACTCTGGTC 480
QY 478 TTCTCCACACGCACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCAAGAG 537
DB 481 TTCTCCACACAGCACTATGTAATGGCCAGGTGATCTGATGACAGCCAGCCCGAG 540
QY 538 AATTTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTCTGGCTT--TCTTTCCC 595
DB 541 CAGTTTGATCATTTCTTCGGCTACAGCATAGTACTGAGCTTAICTGGGTTGTCTTCCC 600
QY 596 TCCTTGTCTATTTGGTGTCTATTTACTGATGGTTCAGGAGCCTGATCAAGCCAGAGAG 655
DB 601 TCCTTGATCATTTCTGGGTGCTACTCTCTGATGGTTCAGGAGCCTGACAAATCCAGTGGAG 660
QY 656 AACTCATAGGACAGGACACAGCCGAGCCAGGTCCATCCGGACCATCTACTCTGTG 715
DB 661 GACCTCCCAACGACAGGCCACAGCCCGGTCGAAGTCTATTGGGACCATCTCTGTG 720
QY 716 TGTGGCTCTTCAACCTCTCTTTTGTGCCCTTCCATATCACTCGCTCTCTTACTCTCAC 775
DB 721 TGTGGCTCTTCAACCTCTCTTTTGTGCCCTTCCATATGCGCGATTTCTTACTTGATC 780
QY 776 ATCTGCTTCTGCTTTCTCAGGACTGCGCAGCTCTTGTATGGCAGCCAGTGTGGCCCTACAAG 835
DB 781 ATCGCTTCTCGAAGTCACAGGACTGCGCAGCTCTTGTGGGCGAGCCAGCATGGCCCTACAAG 840
QY 836 ATATGGAGGCTCTGTGTGAGTGTGAGCAGCTGCGCTCAACCCAGTCTCTTCTTTTCA 895

Db 841 GTCTGAGGCCTCTGGTAAGCATGAGCAGCTGCCCTCAATCCAGTCTGTACTTCTTGICA 900
Qy 896 AGGGG 900
Db 901 CAGGG 905

Search completed: February 15, 2006, 12:35:52
Job time : 652 secs

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